\$TIC-Biotech/ChemLib

From: Sent:

Schnizer, Richard Monday, March 10, 2003 12:11 PM STIC-Biotech/ChemLib 09/836,439

To:

Subject:

Please search the commercial databases for SEQ ID NOS: 1-6 from 09/836,439.

Thank you-

Richard Schnizer, Ph.D. Patent Examiner Art Unit 1635 CM1 12E17 703-306-5441 Mail Box CM1 11E12

Point of Contact: **Toby Port** Technical Info. Specialist CM1 6A04 703-308-3534

Searcher:
Phone:
Location:
Date Picked Up: 3/11
Date Completed: 3/19
Searcher Prep/Review:
Clerical:
Online time:

TYPE OF SEARCH:
NA Sequences:
AA Sequences:
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other

ENDOR/COST (where applic.)
STN:
DIALOG:
Questel/Orbit:
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length 41.2 41.2 40.0 40.0 40.0 40.0 39.7 39.7 39.7 39.7 39.7 7 56043 66991 7 74026 7 80866 7 110000 7 190642 7 208375 7 309357 1 91104 1 160589 8 0 10591 0 73076 0 168540 0 303356 7 3554 DΒ 2 AC012649 3 AC095015_1 3 AC095015_1 3 AC095015_1 2 AC107703 2 AC112364 10 AL663066 6 193656 1 AE008861 1 AE008861 1 AE008861 2 AC094066 2 AC0940666 2 AC109157 2 AC109788 10 AL607109 10 AMPBALT 10 MMPBALT 10 M AC020132 AC003055 AC092189 AE003583 DMFTZ1 AC012761 AC011653 AC101196 AC101196 Mus muscu AC1012649 Drosophil Continuation (2 of AC095015 Drosophil AC107703 Mus muscu AE003673 Drosophil AC107703 Mus muscu AE003674 Rattus no AL663066 Nouse DNA AR024439 Sequence 22 AE008861 Salmonell AL69767 Mouse DNA AC094068 Rattus no AL450399 Mouse DNA AC094066 Homo sapi AC109789 Bos tauru AL607109 Mouse muscu AC109789 Mus muscu AC107789 Mus muscu AC107789 Mus muscu AC107789 Mouse mRNA AC0444131 Anopheles AC065912 Caenorhab AC44131 Anopheles AC065912 Caenorhab AC44131 Anopheles AC095691 Homo sapi AL3407520 Homo sapi AL341469 Sequence AX282833 Sequence AX282833 Sequence AX282839 Sequence AX282839 Sequence AC092189 Drosophil AE003583 Drosophila X00854 Drosophila AC012761 Drosophil AC001653 Drosophil AR024440 Sequence 193657 Sequence 23 Description

ALIGNMENTS

AR024440 Sequence 23 from patent US 5795972. AR024440 AR024440.1 GI:3977734 Unknown. Unknown. Unknown. 1 (bases 1 to 68) Kmiec, E.B. Chimeric mutational vectors having non-natural nucleotides Patent: US 5795972-A 23 18-AUG-1998;
linear PAT 05-DEC-1

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                                                                                                           This sequence was identified as CDM:10212153 by the submitter. For more information on this record e-mail to fly@celera.com. * NOTE: This is a 'working draft' sequence. * This sequence will be replaced
                                                                                                                                                                                      Submitted (30-DEC-1999) Celera Genomics, 45 West Gude Drive,
                                                                                                                                                                                                                                 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 10591)
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                                                                                                                                                                                                                                                   For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www-hgc.lbl.gov/sequence-archive.html) or send email to drosophila@genome.lbl.gov.

This Pl was assembled from the following subclones: 2_cl
(AC001994), 2_bl2 (AC002947), 1_g6 (AC002944), 1_d4 (AC002943),
2_b5, 2_e4 (AC002952), 1_b4, 2_a1, 2_a2, 1_b6 (AC001992), 1_b8
(AC002945), 2_a8 (AC002946), 1_b2 (AC001994), 2_cc (AC001993), 2_d6
(AC002945), 1_b3 (AC001991), 1_d3 (AC002942), 2_a9 (AC001993),
2_c10 (AC002948), 2_g9 (AC002953), 1_g7 (AC001990), 1_b5
(AC001989), 2_c3 (AC002949), 2_h2, 2_c4 (AC002950), 2_b6.
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Unpublished (1997)
2 (bases 1 to 73076)
2 (bases 1 to 73076)
Celniker, S.E., Ashavani, A., Arcaina, T.T., Baxter, E., Doyle, C.M.,
Farfan, D.E., Flanagan, J., Houston, K.A., Hummasti, S.R., Karra, K.,
Kearney, L., Kim, S.H., Ko, C.L., Li, M., Lomotan, M.A., Mazda, P.,
Mckarney, L., Kim, S.H., Ko, C.L., Li, M., Lomotan, M.A., Mazda, P.,
Mok, M.S., Nixon, K., Pacleb, J.M., Park, S., Pfelffer, B., Punch, D.,
Santos, R.F., Snir, E., Stevko, V., Subramanian, S., Towne, B.,
Wan, K. H., Whitelaw, K.R., Yee, A., Zhang, R., Zieran, L.L. and
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AC003055 AC001994 AC002947 AC002944 AC002943 AC002952 AC001992
AC002945 AC002946 AC001988 AC001995 AC002951 AC001991 AC002942
AC001993 AC002948 AC002953 AC001990 AC001989 AC002949 AC002950
AC003055.1 GI:2584828
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (04-NOV-1997) Berkeley Drosophila Genome Project, MS 74-157, Lawrence Berkeley National Laboratory, One Cyclotron R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence submitted by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kimmel, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kimmel, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wan, K.H., Whitelaw, K.R., Yee, A., Zhang, R., Zieran, L.L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster (Subclones in pOT2 from P1 clone DS06332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Berkeley, CA 94720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lawrence Berkeley National Laboratory, MS
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                                                                                          /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/chromosome="2L"
/clone="P1 DS06332 (D91)"
14890 c 15769 g 21214
                                                                                                                                                                                                                                 Location/Qualifiers
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Pred. No. 12;
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COMMENT
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Best Local Similarity
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23 (celniker, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H.,
4 (celniker, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H.,
4 (celniker, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H.,
4 (celniker, S.E., Addams, M.D., D.D., Banzadon, J.D., Banzadon, J.D., Detz, S.M.,
5 (celniker, M., House, D., Banzadon, J., Beeson, K.Y., Busam, D.A.,
6 (celniker, M., House, D., Comp, L.E., Doyle, C., Dresnek, D., Farfan, D.,
6 (celniker, M., House, E., Galle, R.F., Garg, R.S., George, R.A.,
6 (celniker, M., House, J., Hostin, D., Howland, T.J.,
7 (celniker, J., House, J., Li, P., Mattei, B., Moshrefi, A.,
8 (celniker, M., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunoo, J.,
8 (celniker, B., Parela, S., Patel, S., Pfeiffer, B.,
8 (celniker, B., Phouanenavong, S., Pittman, G.S., Puri, V., Richards, S., Scheeler, F.,
8 (celniker, B., Swith, H.O., Rubin, G.M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RS Celniker, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H., Holt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C., Rogers, Y., An, H., Baldwin, D.D., Banzon, J., Beeson, K.Y., Busam, D.A., Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M., Dodson, K., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Farfan, D., Ferriera, S., Frise, E., Galle, R.F., Garg, N.S., George, R.A., Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J., Lbegwam, C., Jalali, M., Kruse, D., Li, P., Mattel, B., Moshrefi, A., McIntosh, T.C., Moy, M., Wurphy, B., Nelson, C., Nelson, K.A., Nunco, J., Pacleb, J., Paragas, V., Park, S., Pattl, S., Pfeiffer, B., Phouanenavong, S., Pittman, G.S., Puri, V., Richards, S., Scheeler, F., Stapleton, M., Strong, R., Swisskas, R., Tector, C., Williams, S.M., Sequencing of Drosophila chromosome 2L, region 22E-22F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (26-JUN-2001) Berkeley Drosophila Genome Project, 64-121, Lawrence Berkeley National Laboratory, One Cyclotron Berkeley, CA 94720, US
On Sep 6, 2001 this sequence version replaced g1:14550291.
                                                                                                                                                                                                   shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email
                                                                                                                                                                                                                                                                                                                                          This sequence was assembled using end sequences from a whole genome
                                                                                                                                                                                                                                                                                                                                                                                   Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720
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1 (bases 1 to 168540)
Celniker, S. E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
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2 (bases 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence submitted by:
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                                                                                                                                                                        bdgp@fruitfly.berkeley.edu.
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/organism="Drosophila melanogaster"
/strain="y; cn bw sp"
/db_xref="taxon:7227"
                                                                                                                                       Location/Qualifiers
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Pred. No. 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93783 TACGTCGCTGAAAGTTTTTCGTTCCTGCCATGTAATTACGAACGCATTCTTTTCAC 93728
Addams, M.D., Celniker, S.E., Holt, R.A., Evans, C.A., Gocayne, J.D., Andams, M.D., Celniker, S.E., Li, P.W., Hoskins, R.A., Galler, R.F., George, R.A., Lewis, S.E., Richards, S., Ashburner, M., Henderson, S.N., Sutton, G.G., Wortman, J.R., Yandell, M.D., Zhang, O., Chen, L.X., Brandon, R.C., Rogers, Y.H., Blazej, R.G., Champe, M., Péalféer, B.D., Wan, K.H., Doyle, C., Baxter, E.G., Helt, G., Nelson, C.R., Gabor Miklos, G.L., Abril, J.F., Agbayani, A., An, H.J., An, H.J., An, H.J., Baxendale, J., Bayraktaroglu, L., Beasley, E.M., Beeson, K.Y., Berman, B.P., Bhandari, D., Ballew, R.M., Beson, K.Y., Benos, P.V., Berman, B.P., Bhandari, D., Ballew, R.M., Chandra, I., Cavley, S., Dahke, C., Davenport, L.B., Dietz, S.M., Bockshan, M.R., Bouck, J.J., Brokstein, P., Brottler, P., Burtis, K.C., Cherry, J.M., Cawley, S., Dahke, C., Davenport, L.B., Dietz, S.M., Dodson, K., Doup, L.E., Downes, M., Dugan, Rocha, S., Dunkoy, B.C., Cherry, J.M., Cawley, S., Dahke, C., Davenport, L.B., Dietz, S.M., Dodson, K., Doup, L.E., Downes, M., Dugan, Rocha, S., Dunkoy, B.C., Dunn, P., Durbin, K.J., Evangelista, C.C., Ferraz, C., Ferriera, S., Fleischmann, W., Fosler, C., Gabrielian, A.E., Garg, N. S., Howland, T.J., Hernandez, J.R., Houck, J., Hostin, D., Helman, T.J., Hernandez, J.R., Houck, J., Hostin, D., Houston, K.A., Howland, T.J., Well, M. H., Degwam, C., Jalali, M., Kalush, F., Karpen, G.H., Ke, Z., Kravitz, S., Kulp, D., Lai, Z., Lasko, P., Lei, Y., Levitsky, A.A., Kez, J., Morries, J., Moshrefila, M., Welson, D.R., Nelson, M., Fittman, G.S., Pan, S., Pollard, J., Puri, Y., Resee, M.G., Milhina, N.V., Mobarry, C., Muzny, D.M., P., Smith, T., Shen, H., Shue, B.C., Siden Klamos, I., Singson, M., Strong, R., Sun, E., Sprabling, A.C., Venter, E., Wang, R., Sun, E., Sprabling, A. C., Stepleton, M., Strong, R., Sun, E., Sprabling, A.C., Turner, R., Weisen, D.A., Weisen, D.A., Woodage, T., Bang, G., Zao, O., A., Ye, J., Yeh, R. F., Zaveri, J. S., Zhan, M., Zhang, G., Zhao, O., Zheng, Y., Zheng, X. H., Zheng, X. H., Zheng, X. H., Zhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 TACGTAGCAGAAAGTTTTTACUUUCUGCUACGTAGGUUGGAAGGGCGCGTTTTCGC 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AE003583 303356 bp DNA linear INV 04-OCT-20 Drosphila melanogaster genomic scaffold 142000013386046 section
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of 16, complete sequence.
AE003583 AE002638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AE003583.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47514 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 303356)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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a 37192 c 36097 g 47737 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="BACR34M11 (D1362)"
/clone_lib="RPCI-98 (Roswell Park Cancer Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /chromosome="2L"
/map="22E-22F"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GI:10727375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40.0%;
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Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 168540;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA
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On Oct 9, 2000 this sequence version replaced gi:7295946.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adams, M.D., Celniker, S.E., Gibbs, R.A., Rubin, G.M. and Venter, C.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10731132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PGQQAAAPPQFGAPQPGYPGQQPGYPPQPGQQPMPGYPPQPGQQLGGPGYPPQPGAGF
PGQPGRPGFNQPPMPGAGNMYQQAPQARRLDPDQMPDFYQWNIDINGKLSGGPFYVNQP
GLLPPLVTTKFVVHDQGMSSPRFILSGLYCLFUNTGDLLKTTALPLTLAUSPLAKYGG
EMEPPIVNFGEMGPIRCNRCKAYMSPNMQFVDAGRRFQCLMCKVTSEVHQNYYQHLDH
TGQRVDKHERPELLLGTYEFLATKDYCRNNTPPEVPAFIFIIDVSYNTVKSGLVHLLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="FLYBASE:FBan0010882"
/db_xref="FLYBASE:FBgn0031408"
/db_xref="FLYBASE:FBgn0031408"
complement(join(971. .1111,1167. .1970,2033. .290)
3158. .3273,3333. .3791,3851. .4822,5231. .5749))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="FLYBASE:FBan0017006"
/db_xref="FLYBASE:FBan001404"
/db_xref="FLYBASE:FBgn0031404"
/complement(join(6055...687,6960...70
7911...8051,8115...8293,8640...9191))
/gene="CG17006"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="mnpumygppptqpqqqpggapppnsggwppqqqqlpqqqppqq
QLppqqqqqpqygappptsaasqpylngnyqqqlatsmgglsyggggganplkppl
pqgapaaabppptgfwqfnswaappptnnnnaafgappptqagsyyngalppssstqqs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(<971. .>5749)
/gene="CG10882"
                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="FLYBASE:FBan0017006"
/db_xref="FLYBASE:FBgn0031404"
complement(join(8119. .8298,8640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(<6055. .>9191)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VIQEILSMDLNQSVSYLYPREIPIHNVVPEETDLPTPVRCTHEKTQEDGAYILENGVH
LFVWLGQALSPDFVQSVFGVQGLQQIALERFNIVPETPLAKRIHGILEQIMKERSRYM
RVRICNNLVAAERQTGERVPFLPRGGPRYRRFRQLRGFPVSHAQGD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TSAGIRPTEFYGHFFMSNTTDVELASIDATKSISIEIKHDDKLAPEENVYLQVALLYT
SCSGQRRLRILNLALRVTTTIADVFKCCDLDAMMLFFAKQACFKLMEHSPKQVKDNLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SQÎKNILKHLPVDQGQDKSKVRVGFITYNSTVHFYNIKSSLAQPQMMVVGDVQEMEMP
LLDGEFICHPEESAAVLDALMEE!PANFADTKEFFIILYPAIQAGUEALKASNAAGKLL
VENGTLPIABAPGKLKMUDDAKLLGTDKEKFYLTPQTTAVNTLGQECVQDGCSVDLFV
VENGTLPIABAPGKLKMUDDAKLLGTDKEKFYLTPQTAVNTLGQECVDLFV
ENNAYIDLATIGQVSRLTGGEVFKYTYFQADVDGKRLIQDIIKNVSRPIAFDAVMRVR
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PPRSGQIPTSGPABSPRGATPGAPGAATPPTTTGPGLBPDLDGGPPLDGG
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AYTGSIYLPRELKSNSWFLEFQSEERTMVAVPTHFFKILVIDKKFAGDTIPYAEAYSP
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                                                                                                                                                                                                                                                                                                                                                                                                                   complement(<20507. .>21253)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(19456. .20193)
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REFERENCE
AUTHORS
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VERSION
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 3554)
Scott, M. P. and Weiner, A. J.
Structural relationships among genes that control development:
sequence homology between the Antennapedia, Ultrabithorax, and
fushi tarazu loci of Drosophila
Proc. Natl. Acad. Sci. U.S.A. 81 (13), 4115-4119 (1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence homology to Antp and Ubx genes; see DMANTP1 and DMANTP2 sequence homology to prokaryotic and pot. yeast DNA-binding domainer to Pabo C.O., Sauer R.T. (1984) A. Rev. Biochem. 53, 293-32 Data kindly reviewed (19-FEB-1986) by A. Laughon.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 3554)
Laughon, A. and Scott, M.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence of a Drosophila segmentation gene: protein structure homology with DNA-binding proteins Nature 310 (5972), 25-31 (1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA binding protein; inverted repeat; segmentation unidentified reading frame.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fruit fly.
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/product="ftz protein"
/product="ftz protein"
/product="GAA5408.1"
/protein_id="CAA5408.1"
/db_xref="GI:7986"
/db_xref="GI:7986"
/db_xref="FLYBASE:FBgn0001077"
/db_xref="SWISS-PROT:P02835"
/translation="MATTNSQSHYSYADNMANYNMYHPHSLPPTYYDNSGSNAYYQNT
SNYHSYOGY YPOESYSESCYYKNNGBQYTTQTYPPYQPTTPPKATKRKAEDDAASII
AAVEERPSTLRALLINPYKKLKYTPDYFYTTVEQVKKAPAVTTKVTASPAPSYDQEYY
TYPTPSASEDVDYLDYYSPQSQTQKLKNGDFATPPFTTPTSLPPLEGISTPPQSPGEK
                                                                                                                                                                                                                  /note="inverted repeat"
join(1021. .1777,1928.
                                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                   translation-"MQDLPQDQLIRKLTSVACTSQS"
                                                                                                                                                                                                                                                                                                       /protein_id="CAA25407.1"
/db_xref="GI:7985"
                                                                                                                                                                                                                                                                                                                                                                  /note="unidentified reading
                                                                                                                                                                                                                                                                                                                                                                                                             'note="inverted repeat"
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/db_xref="taxon:7227"
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Pred. No. 15;
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REFERENCE
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                   Query Match
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                                                                                                                                                                                                                                               Direct Submission
Submitted (03-NOV-1999) Celera Genomics, 45 West Gude Drive,
Rockville, MD, USA
This sequence was identified as CDM:10210082 by the submitter.
For further information on this sequence you may e-mail to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30;
                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                fly@celera.com.
* NOTE: This is a 'working draft' sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HTG; HTGS_PHASE2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster,
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                                                                                                                                                           This sequence will be replaced by the finished sequence as soon as it is the accession number will be preserved.
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                                                                /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
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2862..2867
/note="pot.
a 952 c
                                                                                                                                               Location/Qualifiers
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HENRYITRRRIDIANALSESRQIKIWFQNRRWKSKKDRTLDSSPEHGGAGYTAMLP
PLEARISTATTGAPSVPWYHHHQTTAAYPAYSHSHSHGYGLLNDYPQOQTHQQYDAY
PQQYQQQCSYQQHPQDLYHLS"
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 39.7%;
58.8%;
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831 g 792 t
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Score 27; DB
Pred. No. 17;
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                   Length 56043;
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         BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Poon, L., Sequeira, A., Sethi, H., Snir, E., Svirskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACU01653 Company Acute Company Acute Company C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    archive Web site (http://www.fruitfly.org/sequence/) or send email
to bdgp@fruitfly.berkeley.edu.
p1 library location: 83-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64-121, Lawrence Berkeley National Laboratory, One Cyclotron Road, Berkeley, CA 94720, US Berkeley, CA 94720, US On or before Apr 16, 1999 this sequence version replaced gi:483986 gi:1945589, gi:1103946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Martin,C.H., Arcaina,T.T., Bondoc,M.M., Chiang,A., Critz,P.A.,
Davis,C.A., Doyle,C.M., Ericsson,C.L., Farfan,D.E., Gunning,K.M.,
Houston,K.A., Jaklevic,M.A., Kadner,K.E., Kim,K., Kim,S.F.,
Ko,C.L., Lewis,K.D., Li,M., Lindquist,K.J., Lomotan,M.A.,
Lustre,V.M., Machrus,M.U., Mayeda,C.A., Miguel,T.M., Miller,C.A.,
Mok,M.S., Pacleb,J.M., Patel,S.G., Santos,R.F., Subramanian,S.,
Wan,K.H., Whitelaw,K.R., Yee,A., Yeh,R.T., Yu,C. and Palazzolo,M.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1998)
2 (bases 1 to 66991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ephydroidea; Drosophilidae; Drosophila
1 (bases 1 to 66991)
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DS07876, complete sequence.
AC001653 L49396 L39779 L32657 L32652 L32645 L32656 L32649 L32648 L32637 L39749 L32654 L33639 L32647 L32642 L32635 L32653 L32651 L32636 L32654 L32634 L32646 L32650 L32636 L32643 L32644
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequencing of antennapedia complex, homeotic genes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence submitted by:
Berkeley Drosophila Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (22-APR-1997) Berkeley Drosophila Genome Project, MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Berkeley, CA 94720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lawrence Berkeley National Laboratory, MS 64-121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               relationship to other sequences,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 further information about this sequence, including its location
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
             þ
/Clone="PI DS07876 (D14)"
/Clone_lib="PI library, partial Sau3A in pNS582tet14Ad10"
/note="This sequence has not changed since its original submission on 08/25/1997. It was resubmitted in order to include all secondary accession numbers for the subclones belonging to this clone."
13581 c 13571 g 20274 t
                                                                                                                                                                                                                                                                                                                                                                                                             /strain="y2; cn bw sp"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Drosophila melanogaster"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                               /map="84B1-84B2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1999 this sequence version replaced gi:483988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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Best Local (
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25751 TIGCATAAAGTITTTACTGTTTACTAGTCATTTTGGAAGTGCGTTTGTTGG 2580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Choepel, Y., Colangelo, M., Collins, S., Collynore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Ginde, S., Gord, S., Kells, C., Lancarares, R., Lenders, T., Lehoczky, J., Levine, R., Liu, G., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEvann, P., McKernan, J., McPheeters, R., Meldrim, J., Weneus, L., Mihova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Raymond, C., Retta, R., Rieback, M., Stange-Thomann, N., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Trayis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, T., Zaimer, A., and Zodv, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastlen,V., Boguslavkiy,L., Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus clone RP23-177G5, AC101196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus, clone RP23-177G5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
                                                                                              sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone
                                                                       will be sequenced to completion. In the event that
                                                                                                                                                                                                                                                                                                                                                                   NOTE: This record contains 93 individual
be preserved.
                                 the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 74026)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                          Center project name: L1613
Center clone name: 177_G_5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HTGS_PHASE0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 to 74026)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GI:17059970
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 27;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74026 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    L16139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 3; Length 66991; 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15;
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7878 7977:

6332: contig of 703

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13491 13590; gap of 100 bp 111 length 14294 14392; contig of 703 bp in length 14294 14393; contig of 706 bp in length 15200 15199; gap of 100 bp 15200 15199; gap of 100 bp 15200 15099; contig of 710 bp in length 15910 16009; gap of 100 bp 161009; gap of 100 bp 17516 16709 16808; gap of 100 bp 17516 17615; gap of 100 bp 17516 17616 17616 17616 pp 17616 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1997 20695: contig of 699 bp in length 20696 20795: gap of 100 bp 20796 21456: contig of 661 bp in length 21457 21556: gap of 100 bp
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3114: contig of 698 bp in length
3115 3214: gap of 100 bp
3215 3917: contig of 703 bp in length
3918 4017: gap of 100 bp
4018 4728: contig of 711 bp in length
4729 4828: gap of 100 bp
5529: contig of 701 bp in length
5530 5629: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8783 8782; gap of 700 bp 11 length 9791 9490; contig of 708 bp in length 9491 9590; gap of 710 bp in length 10301 10400; gap of 710 bp in length 10401 11092; contig of 692 bp in length 11093 11192; gap of 100 bp 100 bp 1000 11093 11192; gap of 100 bp 100 bp 1000 11093 11192; gap of 100 bp 100 bp 1000 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6333 6432: gap of 100 bp 6433 7067: contig of 635 bp in length 7068 7167: gap of 100 bp 7168 7167: contig of 710 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 705: contig of 705 bp in length
706 805: gap of 100 bp
1518 1617: gap of 100 bp
1518 2316: contig of 699 bp in length
2317 2416: gap of 100 bp
2317 2416: gap of 698 bp in length
2317 2416: gap of 698 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                            25499: gap of 100 bp 10 length 25499: gap of 100 bp 26187: contig of 688 bp in length 26287: gap of 100 bp 26287: gap of 100 bp 
                                                                            26993: contig of 706 bp in length 7093: gap of 100 bp 727807: contig of 714 bp in length 7907: gap of 100 bp 28609: contig of 702 bp in length 18709: gap of 100 bp 29413: contig of 704 bp in length 29413: contig of 704 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56: gap of 100 bp
22217: contig of 661 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8682: contig of 705 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          yap of 100 bp in length gap of 100 bp
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877: contig of 710 bp in length
gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bp in length
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                                                                В
                                                                                                                                                                                                                                                                        Matches
21 AAAGITITITACUUUCUGCUACGTAGGUUGGAAGGGCGCGTTTT 63
                                                                                                                                                                                                                                                                                                                        Госат
                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43007 43693 contig of 687 bp in length
43694 43793; gap of 100 bp
43794 44495 of 687 bp in length
44495 44594; gap of 100 bp in length
45295 45291; contig of 697 bp in length
45392 46100; contig of 709 bp in length
46201; gap of 100 bp
46897 46996; gap of 100 bp
47883 4782; gap of 100 bp
47883 4782; gap of 100 bp
48480; contig of 686 bp in length
48281 48480; contig of 686 bp in length
48289 49289 48381; gap of 100 bp
48289 49388; gap of 100 bp
50071 50170; gap of 100 bp
50071 50874; contig of 682 bp in length
50875 50974; gap of 100 bp
51684 51783; gap of 100 bp
51684 51783; gap of 100 bp
51784 52495; contig of 709 bp in length
52496 52595; contig of 710 bp
51684 51783; gap of 100 bp
51684 51783; gap of 100 bp
51684 52495; contig of 709 bp in length
52496 52595; contig of 710 bp
51684 52595; contig of 710 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53301 53400: gap of 100 bp
53301 53400: gap of 100 bp
53401 54108: contig of 708 bp 1
54109 54208: gap of 100 bp
54209 54904: contig of 60 bp
54309 54904: contig of 60 bp
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                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         54209 54904: cont
54905 55004: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41296; conti.
41297 41396; amr
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35036 35743: contig of 708 bp in length
35744 35843: gap of 100 bp
35844 36513: contig of 670 bp in length
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39688 39787: gap of 100 bp
39788 40501: contig of 714 bp in length
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30291 30996: contig of 706 bp
30997 31096: gap of 100 bp
31097 31797: contig of 701 bp
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32568 32667: gap of 100 b
32668 33368: contig of 701
33369 33468: gap of 100 b
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1306; gap of 100 bp 13006; gap of 100 bp 13006; gap of 100 bp 1306; gap of 100 bp 13006; gap of 100 bp 13006; gap of 100 bp 100 
                                                                                                                                                                                                                                                                                                            39.78;
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41296: contig of 695 bp
1396: gap of 100 bp
42103: contig of 707 bp
2203: qap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 bp
1897: contig of 701 bp
1897: gap of
32567: contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36513: contig of 670 bp in length 513: gap of 100 bp in length 37323: contig of --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34129: contig of 661 bp in length 229: gap of 100 bp 34935: contig of 670 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  p of 100 bp contig of 696 bp in length
                                                                                                                                                                                                                                     4; Mismatches
                                                                                                                                                                                                                                                                                                      Score 27; DB 2; Length 74026; Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             p of 100 bp
contig of 677 bp in length
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of 670 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bp in length
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                                                                                                                                                                                                                         Indels
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23026 23125; apr

17: gap of 100 bp 23025: contig of 708 bp 25: gap of 100 bp 25: gap of 699 bp 23824: contig of 699 bp

2218 22317:

gap of

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AL Submitted (02-NOV-1999) Drosophila Genome Center, Lawrence Berkeley Submitted (02-NOV-1999) Brosophila Genome Center, Lawrence Herkeley Laboratory, MS 64-121, Berkeley, CA 94720, USA (1994) This sequence version replaced gi:6175114. On Nov 4, 1999 this sequence version replaced gi:6175114 location For further information about this sequence, including its location For further information about this sequence, including its location For further information about this sequence, visit our sequence and relationship to other sequences, please visit our sequence and relationship to other sequences, please visit our send email archive Web site (http://www.fruitfly.org/sequence/) or send email archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu. All contigs in this submission meet the following cutoffs: length >= 200 bases.

* to bdgp@fruitfly.berkeley.edu. All contigs in this sequence record is so including the sequence in this sequence record is a robitrary. Gaps between the contigs are represented as a runs of N, but the exact sizes of the gaps are unknown.

* runs of N, but the exact sizes of the finished sequence the record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC012649 80866 bp DNA linear HTG 04-NOV-1999 Drosophila melanogaster chromosome X clone BACR07N08 (D1121) RPCI-98 07.N.8 map 17D-17E strain Y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 101 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Celliker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, F., Butenhoff, C., Champe, M., Chavez, C., Chew, M., Clesiolka, L., Boyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Hinkle, A., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, F., Karra, F., Lee, B., Lewis, S., Li, P., Ling, H., Moshrefi, A.R., Washrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Richards, S., Sethi, H., Svirskas, R.R., Wan, K.H., Webster, D., Woolley, P., Yang, S., Yee, M., Yu, C. and Rubin, G.M. Sequencing of Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 80866)
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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AC012649.2 GI:6226990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kim, B., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Poon, L., Sequeira, A., Sethi, H., Snir, E., Svirskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
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7: gap of unknown length
1: contig of 747 bp in length
1: gap of unknown length
3: contig of 829 bp in length
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77: contig of 1022 bp in length
57: gap of unknown length
61: contig of 704 bp in length
61: contig of 704 bp in length
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contig of 1015 bp in length
gap of unknown length
contig of 611 bp in length
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contig of 922 bp in
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of 645 bp in l
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of 1103 bp in length
unknown length
of 599 bp in length
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of 763 bp in length
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of 842 bp in length
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of 1128
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of 1138
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of 1329
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of 2042 bp in length

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8 bp in length
n length
9 bp in length

bp in length

bp in length

length length length

length

of 1169 bp unknown of 865 bp in unknown

length

in length

length

length length

length length

unknown

unknown length

qd

length

length

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length

length

in length

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WPCOMMENT
Sequence split into 5 fragments LOCUS AE001572 Accession AE001572 Fragment Name Begin End
                                                                                                             Matches
                                                                          15 TAGCAGAAAGTTTTTACUUUCUGCUACGTAGGUUGGAAGGGCGCGTTTTCG 65
                                                                                                                      Local
                                                               TIGCATAAAGTTTTTACTGTTTACTAGTCATTTTGGAAGTGCGTTTGTTGG 25561
                                                                                                                      Similarity
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                                                                                                                                                 s: gap of unknown length
8: contig of 593 bp in length
9: qap of unknown length
9: qap of "% 518 bp in length
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archive Web site (http://www.fruitfly.org/sequence/) or send to bdgp@fruitfly.berkeley.edu.

email

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COMMENT
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AE001572_2
AE001572_3
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1 (bases I to 100642)

RS Celniker, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H., Holt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C., Rogers, Y., An, H., Baldwin, D., Banzon, J., Beeson, K.Y., Busam, D.A., Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M., Dodson, K., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Farfan, D., Ferritera, S., Frise, E., Galle, R.F., Garg, N.S., George, R.A., Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J., Ibegwam, C., Jalali, M., Kruse, D., Li, P., Mattel, B., Moshrefi, A., McIntosh, T.C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunco, J., Pacaleb, J., Paragas, V., Park, S., Patel, S., Pfelffer, B., Phouanenavong, S., Pittman, G.S., Purl, V., Richards, S., Scheeler, F., Zaveri, J.S., Smith, H.O., Rubin, G.M. and Venter, J.C., Sequencing of Drosophila chromosome 3R, region 84A-84B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15 TAGCAGAAAGTTTTTACUUUCUGCUACGTAGGUUGGAAGGGCGCGTTTTCG 65
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This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence
                                                                                                                                                                                                                                                                                                                                                       Holt,R.A., Evans,C.A., Gocayne,J.D., Amanatides,P.G., Brandon,R.C., Rogers,Y., An,H., Baldwin,D., Banzon,J., Besson,K.Y., Busam,D.A., Carlson,J.W., Center,A., Champe,M., Davenport,L.B., Dietz,S.M., Dodson,K., Dorsett,V., Doup,L.E., Doyle,C., Dresnek,D., Farfan,D., Ferriera,S., Frise,E., Galle,R.F., Garg,N.S., George,R.A., Gonzalez,M., Houck,J., Hoskins,R.A., Hostin,D., Howland,T.J., Lbeywam,C., Jalali,M., Kruse,D., Li,P., Matted,B., Moshrefi,A., McIntosh,T.C., Moy,M., Murphy,B., Nelson,C., Nelson,K.A., Nunoo,J., Pacleb,J., Paragas,V., Park,S., Patcl,S., Felffer,B., Phouanenavong,S., Pittman,G.S., Putl,V., Richards,S., Scheeler,F., Zaverl,J.S., Smith,H.O., Rubin,G.M. and Venter,J.C.
                                                                                                                                      Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720
                                                                                                                                                                                                          Submitted (15-SEP-2001) Berkeley Drosophila Genome Project, MS 64-121, Lawrence Berkeley National Laboratory, One Cyclotron Road, Berkeley, CA 94720, US Sequence submitted by:
                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Celniker, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H.,
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                       Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farro, S., Ferreira, P., FittHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Plerre, N., Gindes, S., Gord, S., Goyette, M., Graham, L., Grand-Plerre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Norbu, C., Mlenga, V., Murphy, T., Naylor, J., Nuyyen, C., Nicol, R., Norbu, C., Mlenga, V., Murphy, T., Naylor, J., Nuyyen, C., Nicol, R., Norbu, C., Norman, G.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Norman, G.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Tralamas, J., Tesfaye, S., Theodore, J., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Santos, C., Schwies, L., Zimmer, A., and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus clone RP23-472H1, WORKING DRAFT SEQUENCE, 8 ordered
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 208375)
3 (bases 1 to 208375)
8 irren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
Barran,N., Bastien,V., Bloom,T., Boguslavkiy,L., Boukhgalter,B.,
Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,
Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Farro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J.,
Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B.,
Gardyna,S., Gord,S., Graham,L., Johnson,R., Jones,C., Kamat,A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC107703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Birren, B., Nusbaum, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC107703.5 GI:22381033
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                                                                                                                                                                                                                                                                                                      Submitted (24-JAN-2002) Whitehead Institute/MIT Center for Genome
                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55773 a
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mmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
(bases 1 to 208375)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 208375)
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/clone_lib="RPCI-98 (Roswell Park Cancer Institute Drosophila melanogaster BAC library, partial EcoRI in pBACE3.6)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="y; cn bw sp"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Drosophila melanogaster"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39290 c 38978 g 56601 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and Lander, E.
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COMMENT
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misc_teature
                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                    source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               * This sequence will be replaced

* This sequence as soon as it is available and

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* the accession number will be preserved.

* 53806 53905; gap of 100 bp

* 53806 53905; gap of 100 bp

* 56170 56269; gap of 100 bp

* 56270 62030: contig of 5761 bp in length

* 62031 62130; gap of 100 bp

* 62031 71647: contig of 9517 bp in length

* 71648 71747; gap of 100 bp

* 71648 71747; gap of 100 bp

* 71648 71747; gap of 100 bp

* 8166: contig of 12419 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (21-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequencing vector: Plasmid; n/a; 100% of reads chemistry: Dye-terminator Blg Dye; 100% of reads Assembly program: Phrap; version 0.960731 consensus quality: 206755 bases at least Q40 consensus quality: 207261 bases at least Q30 consensus quality: 207461 bases at least Q20 consensus quality: 207461 bases at least Q20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality coverage: 11.1 in Q20 bases; agarose-fp Quality coverage: 10.4 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center code: WIBR
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138341 186299
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Insert size: 207675; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                            186400
                                                                                                                                                                                                                                                                                                                                                                                                                86300 186399: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84167 84266: gap of 100 bp
84267 138240: contig of 53974 bp in length
                         vector_side:left"
                                                                clone_end:SP6
                                                                                                                                                                                                          /db_xref="taxon:10090"
/clone="RP23-472H1"
                                                                                                        /note="assembly_tragment
                                                                                                                                                                      /clone_lib="RPCI-23 Female Mouse BAC"
                                                                                                                                                                                                                                                                       /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                         .53805
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    Summary Statistics

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186299: contig of 47959 bp in length
                                                                                                                                                                                                                                                                                                                                                                                p of 100 bp contig of 21976 bp in length.
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Zheng, X.H.,

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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
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Best Local Similarity
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         ORS Adams, M.D., Celniker, S.E., Holt, R.A., Evans, C.A., Gocayne, J.D., Adams, M.D., Celniker, S.E., Li, P.W., Hoskins, R.A., Galle, R.F., George, R.A., Lewis, S.E., Richards, S., Ashburner, M., Henderson, S.N., Suton, G.G., Wortman, J.R., Yandell, M.D., Zhang, C., Chen, L.X., Brandon, R.C., Rogers, Y.H., Blazel, R.G., Champe, M., Peiffer, B.D., Wan, K.H., Doyle, C., Baxter, E.G., Helt, G., Nelson, C.R., Gabor Miklos, G.L., Abril, J.F., Agbayani, A., An, H.J., Andrews-Pfannkoch, C., Baldwin, D., Ballew, R.M., Basu, A., Andrews-Pfannkoch, C., Baldwin, D., Ballew, R.M., Basu, A., Barendale, J., Bayraktaroglu, L., Beasley, E.M., Beeson, K.Y., Benos, P.V., Berman, B.P., Bhandari, D., Bolshakov, S., Borkova, D., Botchan, M.R., Bouck, J., Brokstein, P., Brottier, P., Burtis, K.C., Cherry, J.M., Cawley, S., Dahlke, C., Davenport, L.B., Davies, P., de Pablos, B., Delcher, A., Deng, Z., Mays, A.D., Dew, I., Dietz, S.M., Dodson, K., Doup, L.E., Downes, M., Dugan-Rocha, S., Dunkov, B.C., Pleischmann, W., Fosler, C., Gobriellan, A.E., Garg, N.S., Gelbart, W.M., Glasser, K., Glodek, A., Gong, F., Gorrell, J.H., Gu, Z., Hernandez, J.R., Houck, J., Hostin, D., Houston, K.A., Howland, T.J., Hernandez, J.R., Houck, J., Hostin, D., Houston, K.A., Howland, T.J., Martis, J., Moshrefi, A., Mount, S.M., Mattel, B., McIntosh, T.C., Mortis, J., Moshrefi, A., Mount, S.M., Mattel, B., McIntosh, T.C., Muzny, D., Lai, Z., Lasko, P., Lei, Y., Leity, A.A., Moharry, C., Muzny, D.M., Nelson, D.L., Nelson, D.R., Nelson, K.A., Nixon, K., Sungson, M., Skupski, M.P., Shen, H., Shue, B.C., Siden-Klamos, I., Saunders, R.D., Scheeler, F., Shen, H., Shue, B.C., Stden-Klamos, I., Stapleton, M., Stopski, M.P., Smith, T., Spier, E., Spradling, A.C., Turner, R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster genomic scaffold 142000013386040 section 3 of 5, complete sequence.
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58490 a 45737 c 44986 g 58461 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39.7%;
67.4%;
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Pred. No. 18;
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               On Oct 9, 2000 this sequence version replaced g1:7298860.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (21-MAR-2000) Celera Genomics, 45 West Gude Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Adams, M.D., Celniker, S.E., Gibbs, R.A., Rubin, G.M. and Venter, C.J.
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PAAPETTSSYPGSQQHLSNNNNNGSGNNNNNNNNNNNNNNNNNNNNNNNMGHTNLHGHLQ
QQQSDLMTNLQLHIKQDYDLTAL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTANGSVGSTHSQGHSDHSQMMDLPLQCSSTEDPTNTALGLQELGLKLEKRIEEAVPA
GQQLQELGMRLRCDDMGSENDDMSEEDRLMLDRSPDELGSNDNDDDLGDSDSDEDLMA
ETTDGERIIY PWMKKHYAGVANGSYQPGMEPKRQRTAYTRHQILELEKEFHYNRYLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(<46894. .>70354)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MTASTGHMSGAVGGGAGVGSVGGGGAGGMTGHPHSMHPADMVSDYMAHHHNPHSHSHS
HTHSLJCHHHSNSAISGHQASAGGYSSNYANATPPSHPHSHPHAHPHQSLGYYVHHAP
EFISAGAVHSDPTNGYGPAANVPNTSNGGGGGGSGAVLGGGAVGGSANGYYGGYGGGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  join(14147
23445. .237
                                                                                                                                                                                                                      /product="CT1096"
                                                                                                                                                                                                                                                                                                                                                                                              /note="CG1030"
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from the published sequence for this transcript."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="Dfd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /map="84A5-84A5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Drosophila melanogaster"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .309357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="Dfd"
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/gene="ftz"
/noto-
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                                                                                                                                                                                                                                                             /db_xref="FLYBASE:FBan0001028"
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avsoeinhrtytapnoagdprinshieftlasdckdsketrqtytryqtlelekefhen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YHMGPYGHPYHQFDIHPSQFAHLSA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(<118482. .>223587)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATSTATTGAPSVPVPMYHHHQTTAAYPAYSHSHSHGYGLLNDYPQQQTHQQYDAYPQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /map="84B1-84B1"
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SCKLQAAVGGLGMVPEGGSPPLVDQMSGHHMNAQMTLPHHMGHPQAQLGYTDVGVPDV
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/db_xref="GI:10727115"
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                                                                                                                                                                                                                                             /note="Antp gene product"
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Matches
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mRNA
                                                                             Local Similarity
                                                                 Conservative
                                                                                                                          /db_xref="FLYBASE:FBan0001982"
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join(275368. .275682,275741. .275774,276161. .276630,
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                                                                                39.7%;
58.8%;
                                                                  6; Mismatches
                                                                                Score 27; DB 3; Length 309357; Pred. No. 19;
                                                                    15;
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Search completed: March 17, 2003, 11:24:06 Job time : 920.892 secs

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Run
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2185239 seqs, 1125999159 residues
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

				a					NO.	Result
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6	26.4	4		27	27	28	28	28	re	o
37.6	38.8	38.8	38.8	39.7	39.7	41.2	41.2	41.2	Score Match Length	uerv
533	68	68	68	3785	68	83	68	68	e Match Length DB ID	
24	20	19	18	23	19	20	19	18	BG	
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Oligonucleotide fo	Oligonucleotide SE	Chimeric mutationa	Chimeric repair ve	Drosophila melanoq	Oligonucleotide us	Oligonucleotide SE	Chimeric mutationa	Chimeric repair ve	Description	

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AARS 1458 AARS 1468 AARS 16951 AARS 16951 AARS 16951 AARS 1697 AAR	ABQ51035 ABL38127 AA199525 AAL44063 AAK544063 AAK52451
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ALIGNMENTS

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/note= "RNA nucleotides" misc_feature 5568 /*tag= e	=	/*tag= b /note= "RNA nucleotides" misc_feature	3	Key Location/Qualifiers misc_feature 129	o sapiens.	Synthetic.	hypercholesterolaemia; haemophilia; DNA/RNA hybrid; ss.	sickle cell disease; beta-thalassemia; Gaucher disease; emphysema;	Chimeric repair vector; CRV; treatment; genetic mutation; repair;	Chimeric repair vector (CRV) SC4.	14-MAY-1998 (first entry)		AAV09396;	RESULT 1 AAV09396 ID AAV09396 standard; DNA; 68 BP.

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RESULT 2
AAV12904
ID AAV1
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AC AAV1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This chimeric repair vector (CRV) SC4 is used in comparative studies on CC the experimental use of a CRV SC1 designed to repair the mutation found CC in Sickle cell disease beta-globin and the beta-globin of a HSC. The CRV CC designed to repair the mutation contains a nucleic acid having at most CC one 3' end and one 5' end comprising a segment of unpaired bases (CC disposed. The unpaired bases separate the nucleic acid into a first CC strand and a second strand, comprising a first region and a second region comprising a first region and a second region comprising a first region and the first region having at least 15 nucleotides. Each nucleotide of the first region comprises at least 8 ribonucleotides, which care Watson-Crick paired to 2'-deoxynucleotides, which ribonucleotides form at least least one ribonucleotide segment of at least 3 ribonucleotides cand the sequence of the first or the second region is the sequence of a firagment of a wild-type allele of a human gene. The CRVs can be used for treating diseases. They can be used for treating, sickle cell cliebase, beta-thalassenia, familial hypercholesterolaemia, Gaucher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loc
Matches
                                                                                                                                                                                                                                                      Chimeric mutational vector; alkaline phosphatase gene; gene repair; disease-related mutation; human; Gaucher's disease; sickle-cell anaemia; thalassemia; familial hypercholesterolaemia; emphysema; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric nucleic acid repair vectors - used for treating diseases such as sickle cell disease, beta-thalassemia, Gaucher disease, hyper:cholesterolaemia, emphysema or haemophilia
                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                      Chimeric mutational vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAV12904 standard; DNA; 68 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 68 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 A; 19 C; 19 G; 13 T; 6 U; 0 other;
                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kmiec EB,
   /note= "binds to nucleotides 54 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "DNA nucleotides"
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                                                                                                                                                                                                                                                                                                                                                                                      SC4.
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Pred. No. 0.57;
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RESULT 3
AAX19657

AAX19657 standard;

DNA;

68

ВP

0

PXXXX

AAX19657;

02-JUN-1999

(first entry)

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Ωy
                                                                                                                                                  В
                                                                                                                                                                                                                                                                                           This sequence represents a nucleotide analogue of the invention, termed a chimeric mutational vector (CMV). This sequence is directed against the beta-globin gene. The CMVs (I) are for altering a gene in a cukaryotic cell, and comprise: (a) a first strand (S1) having at least 15 nucleotides (nt); at least 3 nuclease-resistant ribo-type nt (nt') and at least 3 contiguous ribo-type nt, the same as, or additional to, the nt'; and (b) a second strand (S2) in which the nt are Watson-Crick (WC) paired to the nt in S1. The contiguous ribo-type nt in S1 are WC-paired to to the nt in S1. The contiguous ribo-type nt is other than a C2'-0-methyl substituted nt. nt' are 2'-AX-nucleosides; 2'-AX-nucleosides 2'-O-methyl substituted nt. nt' are 2'-AX-nucleosides; 2'-AX-nucleosides C2'-0-methyl substituted nt. nt' are 2'-AX-nucleosides; 2'-AX-nucleosides C2'-C-methyl substituted nt. nt' are 2'-AX-nucleosides; 2'-AX-nucleosides C2'-C-methyl substituted nt. nt' are 2'-AX-nucleosides; 2'-AX-nucleosides C3'-AX-nucleosides; A = oxygen, fluoro, chloro or bromo; when A = O, C3 = hydrogen or 1-6C alkyl and R = 1-6C alkyl; when A is halo then R and C3 are absent. (I) are used to repair a disease-related mutation in human cells (e:g. those associated with Gaucher's disease, sickle-cell anaemia,
                                                                           Matches
                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                   thalassemia, familial hypercholesterolaemia, emphysema etc.). The chimeric mutation vectors are also used to inactivate specific genes, i.e. to generate transgenic ('knockout') animals or plants. They are used for biomedical research and for pharmaceutical production. Any eukaryotic gene of known sequence can be altered, by replacement, deletion or addition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oligonucleotide for altering a genomic sequence in eukaryotes - particularly for correcting disease-related mutation(s) and for production of transgenic animals and plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_RNA
                                                                                                                                                  Sequence 68 BP; 11 A; 19 C; 19 G; 13 T; 6 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 7.2; Fig 3; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-063068/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYJE-) UNIV JEFFERSON THOMAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-DEC-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                    9
 9
                                    CCTACGTAGCAGAAAGTTTTTACUUUCUGCUACGTAGGUUGGAAGGGCGCGTTTTCGCGC 68
CCTGAGGAGAAGACTGCTTTTGCAGUCUUCUCCTCAGGAGUCAGGUGCGCGTTTTCGCGC 68
                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96US-0664487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97WO-US10538
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55..59
/*tag=
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64..68
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30..39
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/*tag=
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                                                                                            41.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "binds to nucleotides 59 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "binds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "binds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ь
                                                                           0,
                                                                                          Score 28; DB 19; Length 68 Pred. No. 0.57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to nucleotides 25
                                                                             Mismatches
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                                                                             20;
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                                                                             0
                                                                         Gaps
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pentaethylene oxide

(PEO)

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RESULT 4
AAAVS2984
ID S2984
AC AAV'
XX
AC AAV'
XX
DT 04-1
DT 04-1
DX
Chi
KW Chi
KW Int.
KW Int.
KW Indeg
KW ONA
XX
OS Syn
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                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local 9
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01-MAY-1996;
17-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes double-stranded oligonucleotides (I) containing fragments of wild-type human alleles. (I) are used to repair disease associated mutations in human cells. (I) are preferably used to treat sickle cell aneemia or thalassemia (mutations in the beta-globin gene, including the promoter region), or Gaucher's disease (mutations in the glucocarebrosidase gene), in haematopoietic cells. (I) may also be used to treat familial hypercholesterolaemia (mutations in the lowdensity lipoprotein receptor gene), emphysema (the alpha 1-anti-trypsin gene), haemophilia (the factor VIII gene) or Christmas disease (the factor IX gene), in hepatocytic cells. (I) provides repair of small genetic mutations. The present sequence represents an oligonucleotide
                                             Chimeric oligonucleotide; specific alteration; target sequence; intramolecular duplex stability; intermolecular duplex stability; intermolecular duplex stability; nuclease degradation; chemical stability; hydrolysis resistance; degradation resisitance; A-type helix formation; stable conformation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Double-stranded oligonucleotides with containing a human wild-type allele - useful for repairing mutations in human cells, particularly those causing sickle cell anaemia or thalassemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome; genetic lesion; haematopoietic stem cell; hepatocyte; RNase; human wild type allele; mutation; sickle cell anaemia; thalassemia; Gauchar's disease; glucocerebrosidase gene; hypercholesterolaemia; emphysema; haemophilia; Christmas disease; ss.
                                                                                                                        Oligonucleotide used in the course of the invention.
                                                                                                                                                          04-DEC-1998
                                                                                                                                                                                         AAV52984;
                                                                                                                                                                                                                    AAV52984 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Column 61-62; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cole-Strauss AD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                           from the present invention.
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                                                                                                                                                                                                                                                                                                                                   ဖ
                                                                                                                                                                                                                                                                                                                    CCTACGTAGCAGAAAGTTTTTACUUUCUGCUACGTAGGUUGGAAGGGCGCGTTTTCGCGC 68
                                                                                                                                                                                                                                                                                                 40;
                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                            BP; 11 A; 19 C; 19 G;
                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JEFFERSON THOMAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97US-0906265.
96US-0640517.
96US-0664487.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kmiec EB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ij
                                                                                                                                                                                                                                                                                                                                                                             41.2%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NO:96.
                                                                                                                                                                                                                      83
                                                                                                                                                                                                                    ВP
                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                             Score 28;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                            13 T;
                                                                                                                                                                                                                                                                                                                                                                             DB 20;
0.57;
                                                                                                                                                                                                                                                                                                                                                                                                                            6 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                               20;
                                                                                                                                                                                                                                                                                                                                                                                            Length 68
                                           stable conformation;
                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                 89
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ABL03968/c
ID ABL039
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                                                                                                                                                                                                                                                                                                                                             В
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                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention provides chimeric oligonucleotides comprising a stem portion having one or more nucleotides selected from 2'-0-alkyl-ribonucleotides, 2'-allyl-ribonucleotides, 2'-halo-ribonucleotides, 2'-o-methoxyethyl-ribonucleotides, 2'-branching group-ribonucleotides, 2'-o-methoxyethyl-ribonucleotides, 2'-branching group-ribonucleotides, and one or more ribonucleotides or 2'-o-branching group-ribonucleotides, and one or more loop portions. The chimeric oligonucleotides may be used for introduction of specific alterations into target nucleic acid sequences located in living organisms. They have increased intramolecular and intermolecular ouplex stability, increased resistance to nuclease degradation and increased chemical stability, resistance to hydrolysis and degradation, as compared to known chimeric oligonucleotides. They have structures which induce intramolecular and intermolecular Artype helix formation. They have highly stable conformations, as measured by thermal melting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 68 BP; 13 A; 17 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 3; Page 33; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
                           Drosophila melanogaster
                                                             pharmaceutical;
                                                                                                         Drosophila
                                                                                                                                        26-MAR-2002
                                                                                                                                                                       ABL03968;
                                                                                                                                                                                                   ABL03968 standard; cDNA; 3785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       measurements.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This oligonucleotide is used in the course of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New chimeric oligo:nucleotide(s) - which are useful for causing specific alterations in target nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-495787/42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9839353-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PEKE ) PERKIN-ELMER CORP
                                                                                                                                                                                                                                                                                  62 TTCGCGC
                                                                                                                                                                                                                                                                                                               62 TTCGCGC
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                                                                                                                                                                                                                                                                                                                                                                             N
                                                                                                                                                                                                                                                                                                                                              CTTCCAACGAGGGATGCTCTACTATTTTAGTAGAGCATCCCTCGTTGGAAGTGCGCGTT
                                                                                                                                                                                                                                                                                                                                                                CTTCCAACCTACGTAGCAGAAAGTTTTTACUUUCUGCUACGTAGGUUGGAAGGGCGCGTT
                                                                                                                                                                                                                                                                                                                                                                                                            39;
                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kuimelis RG;
                                                                                                         melanogaster expressed polynucleotide SEQ ID NO
                                                                         developmental biology;
                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                  83
                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97US-0039244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98WO-US03224
                                                            gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers 26..29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                       39.7%;
58.2%;
                                                             ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "nucleotides replacing loop portion"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 G;
                                                                                                                                                                                                                                                                                                                                                                                                          Ψ
                                                                                                                                                                                                                                                                                                                                                                                                         Score 27; DB 19; Length 68
Pred. No. 1.3;
3; Mismatches 25; Indels
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21 T; 0 other;

0

Gaps

0

cell signalling;

6386

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AAV09395
ID AAV0
XX
AC AAV0
XX Chin
XX Chin
XX Chin
XX Synt
XX Synt
XX Synt
XX Synt
XX Home
XX Synt
YF Mis
FT mis
FT mis
FT mis
FT mis
FT mis
                                                                                                                                                                                                                                                                                                                                                                                 Db
                                                                                                                                                                                                                                                                                                                                                                                                      QΥ
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                  3541
                                                                                                                                                                                              Chimeric repair vector; CRV; treatment; genetic mutation; sickle cell disease; beta-thalassemia; Gaucher disease; er hypercholesterolaemia; haemophilia; DNA/RNA hybrid; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLIG175) and the encoded proteins
                                                misc_feature
                                                                                    misc_RNA
                                                                                                                                                                                                                                             Chimeric repair vector (CRV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid genes from Drosophila and interactions -
            misc_RNA
                                                                                                                         misc_feature
                                                                                                                                                             Homo sapiens.
                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                              AAV09395;
                                                                                                                                                                                                                                                                                                                     AAV09395 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3785 BP; 876 A; 851 C; 982 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 6386; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-MAR-2000;
11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                             2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                    (first entry)
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2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001WO-US09231
                                               /note=
40..44
                                                                      /note=
30..39
/*tag=
 /*tag=
/note=
45..54
/*tag=
                                                                                                       /*tag=
                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                      DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                          39.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ŀ
                                                            "RNA
                                                                                               "DNA
                         "DNA nucleotides
 a
                                      a
                                                                                                                                                                                                                                                                                                                      68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      detection reagent for detecting for elucidating cell signalling
                                                                                                                                                                                                                                                                                                                      ВP
                                                                                                 nucleotides"
                                                                                                                                                                                                                                                                                                                                                                                                                                6,
                                                            nucleotides
                                                                                                                                                                                                                                                SC3.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 27;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1076 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 23; Length 3785;
                                                                                                                                                                                                                                                                                                                                                                                                                                15;
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                                                                                                                                                                                                         emphysema
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1000 or more and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Synthetic.

Location/Qualifiers

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RESULT 7
AAV12903
ID AAV12903
XX
AC AAV1
XX
DT 17--
DT 17--
DK Chin
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CKW Chin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    one 3' end and one 5' end comprising a segment of unpaired bases disposed. The unpaired bases separate the nucleic acid into a first strand and a second strand, comprising a first region and a second region respectively, each region having at least 15 nucleotides. Each nucleotide of the first region is Watson-Crick paired to a nucleotide of the second region and the first region comprises at least 8 ribonucleotides, which are Watson-Crick paired to 2'-deoxynucleotides, which ribonucleotides form at least one ribonucleotide segment of at least 3 ribonucleotides and the sequence of the first or the second region is the sequence of a fragment of a wild-type allele of a human gene. The CRVs can be used for repairing genetic mutations in cells for re-introducing into a patient for treating diseases. They can be used for treating, sickle cell disease, beta-thalassemia, familial hypercholesterolaemia, Gaucher
                                                                                                     Chimeric mutational vector; alkaline phosphatase gene; gene repair; disease-related mutation; human; Gaucher's disease; sickle-cell ana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chimeric nucleic acid repair vectors - used for treating diseases such as sickle cell disease, beta-thalassemia, Gaucher disease, hyper:cholesterolaemia, emphysema or haemophilia
                                                                                                                                                          Chimeric mutational vector SC3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This chimeric repair vector (CRV) SC3 is used in comparative studies on the experimental use of a CRV SC1 designed to repair the mutation found in Sickle cell disease beta-globin and the beta-globin of a HSC. The CRV designed to repair the mutation contains a nucleic acid having at most
                                                                                     thalassemia;
                                                                                                                                                                                            17-JUN-1998
                                                                                                                                                                                                                               AAV12903;
                                                                                                                                                                                                                                                                AAV12903 standard; DNA; 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 3; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cole-strauss A, Kmiec EB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYJE-) UNIV JEFFERSON THOMAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-1996;
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                                                                                                                                                                                                                                                                                                                                                       CCTGAGGAGAAGACTGCTTTTGCAGUCUUCUCCTCAGGAGUCAGAUGCGCGTTTTCGCGC 68
                                                                                                                                                                                                                                                                                                                                                                                    CCTACGTAGCAGAAAGTTTTTACUUUCUGCUACGTAGGUUGGAAGGGCGCGCTTTTCGCGC 68
                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          emphysema or haemophilia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 BP; 12 A; 18 C;
                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                           (first
                                                                                       familial hypercholesterolaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96US-0640517.
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/note=
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                                                                                                                                                                                            entry)
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                                                                                                                                                                                                                                                                  ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 18; Length
                                                                                       emphysema; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                        21;
                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           68;
                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                         anaemia;
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CC This sequence represents a nucleotide analogue of the invention, termed a chimeric mutational vector (CMV). This sequence is directed against the continuous cell, and comprise: (a) a first strand (S1) having at least 15 cc eukaryotic cell, and comprise: (a) a first strand (S1) having at least 15 cc nucleotides (nt); at least 3 nuclease-resistant ribo-type nt (nt') and at least 3 contiguous ribo-type nt, the same as, or additional to, the nt'; cc and (b) a second strand (S2) in which the nt are Watson-Crick (WC) paired to the nt in S1. The contiguous ribo-type nt in S1 are WC-paired to cc 2'-deoxyribo-type nt, and at least one ribo-type nt is other than a cc 2'-o-methyl substituted nt. nt' are 2'-Ax-nucleosides; 2'-Ax-nucleosides or 2'-AR-nucleotides; A - oxygen, fluoro, chloro or bromo; when A = 0, cc X - hydrogen or 1-6c alkyl and R = 1-6c alkyl; when A is halo then R and cells (e.g. those associated with Gaucher's disease-related mutation in human cells (e.g. those associated with Gaucher's disease, sickle-cell anaemia, thalassemia, familial hypercholesterolaemia, emphysema etc.). The collineric mutation vectors are also used to inactivate specific genes, i.e. to generate transgenic ('knockout') animals or plants. They are also used for biomedical research and for pharmaceutical production. Any eukaryotic gene of known sequence can be altered, by replacement,
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                                          S
                                                                                                                                       Query Match
                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oligonucleotide for altering a genomic sequence in eukaryotes particularly for correcting disease-related mutation(s) and for production of transgenic animals and plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
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                                                                                                                                                                                         Sequence 68 BP; 12 A; 18 C; 18 G; 14 T; 6 U; 0 other;
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                      CCTACGTAGCAGAAAGTTTTTACUUUCUGCUACGTAGGUUGGAAGGGCGCGTTTTTCGCGC
CCTGAGGAGAAGACTGCTTTTGCAGUCUUCUCCTCAGGAGUCAGAUGCGCGTTTTCGCGC
                                                                                                                   Similarity
                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JEFFERSON THOMAS
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                                                                                          Score 26.4; DB 19; Length Pred. No. 2.2; Indels 0; Mismatches 21; Indels
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Matches 39
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01-MAY-1996;
17-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genome; genetic lesion; haematopoletic stem cell; hepatocyte; RNase human wild-type allele; mutation; sickle cell anaemia; thalassemia; Gaucher's disease; glucocerebrosidase gene; hypercholesterolaemia; emphysema; haemophilia; Christmas disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                              containing fragments of wild-type human alleles. (I) are used to repair disease associated mutations in human cells. (I) are preferably used to treat sickle cell anaemia or thalassemia (mutations in the beta-globin gene, including the promoter region), or Gaucher's disease (mutations in the glucocerebrosidase gene), in haematopoietic cells. (I) may also be used to treat familial hypercholesterolemia (mutations in the low-density lipoprotein receptor gene), maniphysema (the alpha 1-anti-trypsin gene), haemophilia (the factor VIII gene) or Christmas disease (the factor IX gene), in hepatocytic cells. (I) provides repair of small genetic mutations. The present sequence represents an oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oligonucleotide SEQ ID NO:95
Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism SNP; cell differentiation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Double-stranded oligonucleotides with containing a human wild-type allele - useful for repairing mutations in human cells, particularly those causing sickle cell anaemia or thalassemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cole-Strauss AD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-AUG-1997;
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                                                                                    Oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes double-stranded oligonucleotides (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Column 59-60; 40pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    the present invention.
                                                                                                                                                                                                                                                                   CCTGAGGAGAAGACTGCTTTTGCAGUCUUCUCCTCAGGAGUCAGAUGCGCGCTTTTCGCGC 68
                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                   BP; 12 A; 18 C;
                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                 (first entry)
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96US-0664487.
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                                                                                  for detecting cytosine methylation SEQ
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Pred. No. 2.2;
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methylation of a particular cytosine in a motif 5'-Cpg-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic CD NA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one commenter, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the classes of oligomers, the degree of methylation is calculated. The method classes of oligomers, the degree of methylation is calculated. The method the respective of the central nervous, cardiovascular, gastrointestinal and respiratory composition of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc. particularly by detecting mutations or single nucleotide composition status of many C residues to be determined simultaneously. ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the method disclosure of the invention.
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                                                                                                                                                                                                                                                      RESULT 10
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                                         Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.
                                                                                                                                                         12-JUL-2002
                                                                                                                                                                                                                     ABQ51035 standard; DNA; 533
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 533 BP; 89 A; 62 C; 208 G; 174 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 12; 56pp + Sequence Listing; 56pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Determining the degree of cytosine methylation in genomic DNA, for diagnosis and prognosis, comprises selective hybridization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-SEP-2000; 2000DE-1043826.
05-SEP-2000; 2000DE-1044543.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-SEP-2001; 2001WO-EP10074.
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                                                                                                                                                                                                                                                                                                                 12 ACGTAGCAGAAAGTTTTTACUUUCUGCUACGTAGGUUGGAAGGGCGCGTTTTCGCG
                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                       μ.
                                                                                                                                                                                                                                                                                                   ATGTCGCGGGATTTTTTTTTTTTTTTTTTTGTAGGAAGGTTGGAAGCGCGAGATTTAGGG
                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from chemically treated
                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                      (first entry)
                                                                                                                    for detecting cytosine methylation SEQ ID NO 37626.
                                                                                                                                                                                                                                                                                                                                                                                37.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Berlin
                                                                                                                                                                                                                       ₿₽
                                                                                                                                                                                                                                                                                                                                                                 6;
                                                                                                                                                                                                                                                                                                                                                                                Score 25.6; DB 24; Length Pred. No. 7.1;
                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ζ,
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                                                                                                                                                                                                                                                                                                                                                                 19;
                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                               0;
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This invention describes a novel method for determining the degree of CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a CC genomic sample of DNA. The sample is treated chemically to convert CC genomic Sample of DNA. The sample is treated chemically to convert CC CYtosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. CC The amplicon is hybridised to two classes, each with at least one member, of oligonuclectides and/or peptide-nucleic acid (PNA) oligomers CC and the degree of hybridisation to both classes is determined from the clabel on the amplicon. From the ratio of labels hybridised to the two CC classes of oligomers, the degree of methylation is calculated. The method is used: (1) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders CC therapeutic particularly by detecting mutations or single nucleotide CC systems etc., particularly by detecting mutations or single nucleotide CC types and for investigating cell differentiation of cell or tissue CC types and for investigating cell differentiation. The method allows the CC methylation status of many C residues to be determined simultaneously. ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the company of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-SEP-2000;
05-SEP-2000;
                                           the disclosure of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 12; 56pp + Sequence Listing; 56pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amplicons from chemically treated DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-371829/40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-SEP-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200218632-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000DE-1043826
2000DE-1044543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001WO-EP10074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Guetig
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Sequence 533 BP; 174 A; 208 C; 62 G; 89 T; 0 other;

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Matches
                                                               Query Match
Best Local :
533 ATGTCGCGGGATTTTTTTTTTTTTTTTTTTTTTTTGTAGGAAGGTTGGAAGCGCGAGATTTAGGG 478
                       12 ACGTAGCAGAAAGTTTTTACUUUCUGCUACGTAGGUUGGAAGGGCGCGTTTTCGCG 67
                                                              Local
                                                               Similarity
                                                   Conservative
                                                              37.6%;
                                                 6,
                                               Pred. No. 7.1;
6; Mismatches
                                                            Score 25.6;
Pred. No. 7
                                                                          DB
                                                 19;
                                                                          24;
                                                                         Length 533;
                                                Indels
                                                 0
                                                 Gaps
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RESULT 11 ABL38127 standard; cDNA;

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ABL38127;

08-APR-2002

Human colon tumour antigen polynucleotide SEQ ID NO:1716 (first entry)

Human; colon cancer; colon tumour antigen; cytostatic; vaccine; tumour metastatic antigen; diagnosis;

WO200196388-A2

ABL38127
XX
AC ABL3
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AC ABL3
XX
DT 08-A
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08-JUN-2001; 2001WO-US18557.

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RESULT 12
AAI99525/c
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Best Local :
          31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
19-MAY-2000;
19-MAY-2000;
07-JUN-2000;
30-JUN-2000;
07-JUN-2000;
                                                                                                                                                                                                                                       Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
                                                                                                                                                  17-JAN-2001; 2001WO-US01356
                                                                                                                                                                                                 WO200155173-A2
                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                  neurological disease; infection; human; secreted protein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABL36412 to ABL38645 represent human colon tumour antigen cDNA clones (I) which were isolated from human colon tumour and colon metastatic tumour cDNA libraries. (I) have cytostatic activity and can be used in vaccine production. (I) can be used for stimulating and/or expanding T cells specific for a tumour protein on contact with the T cells. They are also useful for inhibiting the development of cancer in a patient. (I) can be mutant species primers for nucleic acid hybridisation, for preparing can be used in the diagnosis of a colon tumour.
                                                                                                                                                                                                                                                                                                           Human
                                                                                                                                                                                                                                                                                                                            07-JAN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                       AAI99525 standard; cDNA; 1280 BP.
                                                                                                                                                                                                                                                                                                                                                       AAI99525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 435 BP; 114 A; 98 C; 91 G; 130 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID 1716; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel isolated colon tumor polynucleotide differentially expressed in colon tumor or colon metastatic tumor and polypeptides encoded by them, useful for inhibiting development of cancer in patient -
                                                                                                                                                                                                                                                                                                                                                                                                                        09-JUN-2000; 2000US-210899P.
20-FEB-2001; 2001US-270216P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-114514/15.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             2 CTTCCAACCTACGTAGCAGAAAGTTTTTACUUUCUGCUACGTAGGUUGGAAGGGCGCGT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OCAL
                                                                                                                                                                                                                                                                                                        polynucleotide SEQ ID NO 23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
        2000US-0179065
2000US-0180628
2000US-0184664
2000US-0186350
2000US-0189874
2000US-01990076
2000US-0199123
2000US-0205515
2000US-020467
2000US-0214886
2000US-0214886
2000US-021647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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55.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 25.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DВ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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02-0CT-2000;
02-0CT-2000;
02-0CT-2000;
02-0CT-2000;
02-0CT-2000;
13-0CT-2000;
13-0CT-2000;
20-0CT-2000;
20-0CT-2000;
                                                                                                                                     21-SEP-2000
21-SEP-2000
25-SEP-2000
25-SEP-2000
25-SEP-2000
27-SEP-2000
27-SEP-2000
29-SEP-2000
29-SEP-2000
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29-SEP-2000
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08-SEP-2000;
08-SEP-2000;
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08-SEP-2000;
08-SEP-2000;
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14 - AUG - 2000

18 - AUG - 2000

22 - AUG - 2000

22 - AUG - 2000

23 - AUG - 2000

23 - AUG - 2000

30 - AUG - 2000

01 - SEP - 2000
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14-SEP-2000;
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14-SEP-2000;
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14-SEP-2000;
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06-SEP-2000;
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11-JUL-2000;
       2000US-0241785.
2000US-0241786.
2000US-0241787.
                                     2000US-0239935
2000US-0239937
2000US-0240960
2000US-0241221
                                                                                           2000US-0237037.
2000US-0237038.
2000US-0237039.
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2000US - 0232397
2000US - 0232399
2000US - 0232400
2000US - 0232400
2000US - 0233064
2000US - 0233064
2000US - 0234274
2000US - 0234274
2000US - 0234274
2000US - 0234998
2000US - 0234998
2000US - 0235834
2000US - 0235834
2000US - 0235836
2000US - 0235836
2000US - 02363680
2000US - 02363680
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2000US - 02363680
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2000US-02292887
2000US-0229343
2000US-0229343
2000US-0229345
2000US-022959
2000US-022959
2000US-023943
2000US-0239438
2000US-023143
2000US-0231243
2000US-0231243
2000US-0231243
2000US-0231243
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2000US-0226681.
2000US-0226868.
2000US-0227182.
2000US-0227009.
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2000US-0225268
2000US-0225270
2000US-0225447
2000US-0225757
2000US-0225758
2000US-0225758
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2000US-0225214.
2000US-0225266.
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2000US-0224518.
2000US-0224519.
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2000US-0218290.
2000US-0220963.
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2000US-0217487
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08-NOV-2000;
08-NOV-2000;
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08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
17-NOV-2000;
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08-NOV-2000;
08-NOV-2000;
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20-OCT-2000;
01-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-NOV-20
The invention relates to novel human polynucleotides (AAI99513-AAI99538) and the encoded proteins (AAM99915-AAM99934) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease,
                                                                                                                           Claim 1; SEQ ID NO 23; 465pp + Sequence Listing; English
                                                                                                                                                            New nucleic acids and polypeptides, useful for treating, preventing
                                                                                                                                                  ameliorating human disorders and diseases
                                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                   2001-451924/48.
                                                                                                                                                                                         AAM99927
                                                                                                                                                                                                                            Barash SC,
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2000US-0251868.
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impaired glucose tolerance; insulin resistance; Syndrome X; Type II diabetes; hyperlipidaemia; atherosclerosis; hypertension; and heart

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Best Local :
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1280 BP; 345 A; 277 C; 257 G; 398 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human genset metabolic gene (GMG-7A) cDNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAL44063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAL44063 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                impaired glucose tolerance; insulin resistance; Syndrome X;
Type II diabetes; hyperlipidaemia; atherosolerosis; hypertension;
heart disease; cardiac insufficiency; coronary insufficiency;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-SEP-2002
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                                                                                                                                                                                                                                                                                                                                                                                                   WO200255694-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     non-insulin dependent diabetes mellitus.
                                                                                                                                   Treating or preventing a metabolic-related disease or disorder, ecobesity, impaired glucose tolerance, insulin resistance, Syndrome Type II diabetes, comprises administering Genset Metabolic Genes
                                                                                                                                                                                                                                                                                                        16-JAN-2001; 2001US-262235P.
                         The invention comprises the amino acid and coding sequences of six human genset metabolic genes (GMG-7A, GMG-7B, GMG-8, GMG-9, GMG-10 and GMG-11). The GMG DNA and protein sequences of the invention are useful for treating or preventing metabolic-related disorders, such as: obesity;
                                                                                                      Disclosure; Page 113-116; 128pp; English.
                                                                                                                                                                                                                                                                                                                                          15-JAN-2002;
                                                                                                                                                                                                P-PSDB; AAO15420
                                                                                                                                                                                                                                               Erickson MR, Bour BA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 CTTCCAACCTACGTAGCAGAAAGTTTTTACUUUCUGCUACGTAGGUUGGAAGGGCGCGT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      blood pressure; insulin sensitiser;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33;
                                                                                                                                                                                                                    2002-557821/59.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene; ss; gene therapy; genset metabolic gene; GMG-7A; GMG-7B;
GMG-9; GMG-10; GMG-11; metabolic-related disorder; obesity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                            2002WO-IB01215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers 37..2169
                                                                                                                                                                                                                                                                                                                                                                                                                                  /product= "Human GMG-7A protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA; 2257 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37.4%;
                                                                                                                                                                                                                                                   Bihain B,
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 22;
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RESULT 14
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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polypeptides are useful in gene therapy, vaccines or e.g. stem cell growth factor activity, haematopolesis regulating activity, tissue growth factor activity, haematopolesis regulating activity, tissue growth factor activity, haematopolesis and/or activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
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                                                                                                                                                                        Claim 1; Page 4386-4387; 6221pp; English.
                                                                                                                                                                                                           useful in diagnosis and
                                                                                                                                                                                                              Nucleic acids encoding polypeptides with cytokine-like activities,
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01-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nervous system disorder; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-JUN-2000;
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tissue growth factor; immunomodulatory; cancer; leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human polynucleotide SEQ ID NO 1980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAK52451 standard; cDNA; 2454 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diseases (e.g. cardiac insufficiency, coronary insufficiency or high blood pressure). The GMG DNA and protein sequences of the invention may also be used as insulin sensitisers - for improving insulin sensitivity in persons with non-insulin dependent diabetes mellitus. The present cDNA sequence encodes the human GMG-7A protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2257 BP; 728 A; 522 C; 482 G; 525 T; 0 other;
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Wang D, Wang J, Zhang J, Ren F, C
Yang Y, Wejhrman T, Goodrich R;
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2000US-0560875
2000US-0598075
2000US-0630325
2000US-0654936
2000US-0654936
2000US-0653325
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55.98;
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Pred. No. 12;
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                 The invention relates to polynucleotides (AAKS1456-AAKS3435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polypeptides are useful in gene therapy, vaccines or e.g. stem cell growth factor activity, haematopolesis regulating activity and may be useful in the diagnosis and/or treatment of cancer lankamia narrows such the diagnosis and/or treatment of cancer lankamia narrows such that diagnosis and/or treatment of cancer lankamia narrows such that diagnosis and/or treatment of cancer lankamia narrows such that diagnosis and/or treatment of cancer lankamia narrows such that diagnosis and/or the diagnosis and diagnosis 
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01-SEP-2000;
15-SEP-2000;
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                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy -
treatment of cancer, leukaemia, nervous system disorders, arthritis and
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Xue AJ, Yang Y, Wejhrman T,
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Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAM79319
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tissue growth factor; immunomodulatory; cancer; leukaemia;
nervous system disorder; arthritis; inflammation; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2175 CTTCTGAACAACTTAGGAGAAACTTTTGATCTTCAGCTTGGTAGATTTAATTGCCCAGT 2233
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2000US-0620325
2000US-0634936
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Thom J, Zhang J,
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nang J, Ren F, Chen
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Pred. No. 12;
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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25.8	25.8	25.8	25.8	27	27	esult No. Score
37.9	37.9	37.9	37.9	39.7	39.7	Query Match
923	899	747	741	1101	818	% Query Match Length DB
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в0937919	BQ946406	BI733738	в1739136	CNS0034I	BG188346	% Query Match Length DB ID
BQ937919 AGENCOURT	BQ946406 AGENCOURT	BI733738 603352352	BI739136 603361404	AL063844 Drosophil	BG188346 RST7364 A	Description

ALIGNMENTS

FEATURES	JOURNAL MEDLINE COMMENT		OKGANISM REFERENCE AUTHORS	ITION SION ON RDS E	RESULT 1 BG188346 LOCUS
ACHERSYS, INC. 3201 Carnegie Ave, Cleveland, OH 44115, USA Tel: 216 431 9900 Fax: 216 361 9596 Email: scain@athersys.com High quality sequence stop: 440. Location/Qualifiers	ACLIVATION OI 9ene expression Nat. Biotechnol. 19 (5), 440-445 (2001) 21227151 Contact: Scott J. Cain	Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Boozer, S., Mays, R., Smith, E., Veloso, N., Kilka, A., Hess, J., Cothren, K., Lo, K., Offenbacher, J., Danzig, J. and Ducar, M. Creation of genome-wide protein expression libraries using random	Homo sapiens Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 818) Harrington, J. J. Sherf. B., Rundlett. S., Jackson, P.D., Perry, R.,	Athersys RAGE Library Homo sapiens cDNA, mRh .1 GI:13710033	BG188346 818 bp mRNA linear EST 21-APR-2001

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RESULT 2
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15 TAGCAGAAAGTTTTTACUUUCUGCUACGTAGGUUGGAAGGGCGCGTTTTCG 65
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                                                                                                                                                                                                                                                                                                                                    Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Oscegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be Location/Qualifiers
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AL063844.1 GI:4941600
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                                                                                                                                                                             349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo.sapiens"
//db_xref="taxon:9606"
//db_xref="taxon:9606"
//clone_lib="Athersys RAGE Library"
//cell_line="HT1080"
//note="See 'Creation of Genome-wide Protein Expression / note-"see 'Creation of Genome-wide Protein Expression',
Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

18 a 197 c 181 g 222 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genomic survey sequence.
                                                                                                                                                                      /clone_lib="RPCI-98"
/note="end : TET3"
179 c 216 g
                                                                                                                                                                                                                                                                                                                             1. .1101
                                                                                                                                                                                                                                                                            /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                /clone="BACR07N08"
                                                                       39.7%;
58.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39.7%;
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                                                                          Score 27;
Pred. No.
                                                   Mismatches
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                                                                                                                                                                           325
                                                                          DB
19;
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                                                   15;
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                                                                                            Length 1101;
                                                                                                                                                                        32
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                                                   Indels
                                                                                                                                                                        others
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REFERENCE
AUTHORS
TITLE
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BI733738/c
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AUTHORS
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BI739136/c
LOCUS
                                                                                                                                                                                                                                           DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
VERSION
COMMENT
                                                                                                                                                   SOURCE
                                                                                                                                                                  KEYWORDS
                                                                                                                                                                                                        ACCESSION
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                                                                                                                                                                                        VERSION
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ORGANISM
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                                                                                                                               ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                             368
                                                                                                                                                                                                                                                                                                                                                                                              30 ACUUUCUGCUACGTAGGUUGGAAGGGCGC 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                           ACTTTCTGCTACGTAGGTTGGAAGGCCAC
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                 BI733738 747 bp mRNA linear EST 20-5EF-20 603352352F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:5389908 5',
                 Unpublished (1999)
                                                                                        Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                             Mus musculus
                                                                                                                                                                                      BI733738.1
                                                                                                                                                                                                        mRNA sequence
BI733738
                                                                                                                                                   house mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 741)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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333361404F1 NIH_MGC_94 Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="retina"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Rverage insert size 3.3 %b. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
177 c 194 g 160 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="NIH_MGC_94"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Mus musculus"
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                                                                                                                                                                                      GI:15710751
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   37.9%;
69.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 25.8;
Pred. No. 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                           340
                                                                                        Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB
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                                   Gene
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                                                                                        Euteleostomi;
Murinae; Mus
                                                                                                                                                                                                                                                               EST 20-SEP-2001
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RESULT 5
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Best Local
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                                                                                                                                                                                                                         source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183 ACTITCTGCTACGTAGGTTGGAAGGCCAC 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30 ACUUUCUGCUACGTAGGUUGGAAGGGCGC 58
                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://lmage.llnl.gov
plate: LLAMJ3993 row: 1 column: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleoston Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; N 1 (bases 1 to 899) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                         High quality sequence stop: |
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BQ946406
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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Tissue Procurement: The Cepko Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BQ946406.1 GI:22361884
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Plate: LLAM11915 row: g column: 13
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/db_xref="taxon:10090"
/clone=TiMaGE:5359908"
/clone_lib="NIH_MGC_94"
/tlssue_type="retina"
/tlssue_type="retina"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye: Vector: pCMV-SFORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Librarry enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
18 a 169 c 198 g 162 t
                    /db_xref="taxon.10090"
/clone="IMAGE:6467512"
/clone=1b="NIH_MCC_94"
/tissue_type="retina"
/tissue_type="retina"
/lab_host="hH10B (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally; oligo-dT prime
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  Average insert size 3.3 kb. Library enriched for
                                                                                                                                                                                              /organism="Mus musculus"
                                                                                                                                                                                                                         . 899
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 25.8;
Pred. No. 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                       614.
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Mus musculus cDNA clone IMAGE:6467512
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                         ACCESSION
                                                                                                                                             RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGIN
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VERSION
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                                                                                                Locus
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밁 S BASE COUNT ORIGIN

Matches

FEATURES

FEATURES

COMMENT

JOURNAL

REFERENCE

AUTHORS TITLE

SOURCE KEYWORDS

ORGANISM

DEFINITION ACCESSION

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REFERENCE
AUTHORS
TITLE
                                                           DEFINITION
                                                                                                BG262012/c
                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
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BQ937919/c
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Matches 2
                                                                                                                                                                                                                                                                                                             Query Match
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                                                         602373843F1 NIH_MGC_94 Mus musculus cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM13989 row: d column: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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BG262012.1 GI:12771828
                     BG26201
                                      mRNA sequence.
                                                                               BG262012
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Mammalia; Eutheria; Rodentia;
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/db_xref="taxo":10090"
/clone="nMAGE:6465857"
/clone="lib="NIH_MGC_94"
/tlssue_type="retina"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
/site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
51 a 224 c 233 g 214 t 1 others
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Note: this is a NIH_MGC Library."
208 c 231 g 207 t 5 others
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Pred. No. 50;
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Pred. No. 50;
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                                                           IMAGE: 4481291
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACTITCTGCTACGTAGGTTGGAAGGCCAC 443
                              DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAMI0318 row: a column: 16
                                                                                                                                                                                                                                                                              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; 1 (bases 1 to 961)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
                                                                                                                                                                                                                                             Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                      house mouse.
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                       BG342737.1 GI:13149175
EST.
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Location/Qualifiers
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house mouse
                High quality sequence stop: 653.
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http://image.llnl.gov
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/tissue_type="retina"
/lab_host="DH10B (phage-resistant)"
/note="organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NHH_MGC Library."
a 230 c 256 g 188 t
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/clone="IMAGE:4481291"
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Pred. No. 51;
7; Mismatches
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                 Plate: LLAM10376 row: 1 column: High quality sequence stop: 735.
                                                                                                                                                                                                                                                                                                                                                                                                          found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM10376 row: 1 column: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
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Similarity 69.0
20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            house mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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                                                                 /clone_lib="NII_MOV__.
/tissue_type="retina"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: Note_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
Note: this is a NIH_MGC Library."
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/tissue_type="retina"
/tissue_type="retina"
/lab_host="hH108 (phage-resistant)"
/note="Organ: eye; Vector: pcMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
a 218 c 254 g 201 t
                                                                                                                                                                                                                                                                /organism="Mus musculus"
/db_xref="taxon:10000"
/clone="IMAGE:4504476"
/clone_lib="NIH_MGC_94"
                                                                                                                                                                                                                                                                                                                                                     1. .1101
                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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/clone="IMAGE:4481943"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
                     37.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37.9%;
                     Pred.
                                        Score 25.8;
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Pred. No. 51;
  Mismatches
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                     No.
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E:4504476 5',
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30 ACUUUCUGCUACGTAGGUUGGAAGGGCGC

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76 ACTITCTGCTACGTAGGTTGGAAGGCCAC 48

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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                 305-8602, Japan
Tel: 81-298-38-7441
Fax: 81-298-38-7468
                                                                     Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome_Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
                                                                                                                                                                                                             oryza sativa (japonica cultivar-group).
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Enrharcoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                        AU096979
AU096979 Rice green shoot Oryza sativa (japonica cultivar-group)
cDNA clone S16784, mRNA sequence.
                                                                                                                                               Rice cDNA from green shoot (2000) Unpublished (2000)
                                                                                                                                                                                 Sasaki, T. and Yamamoto, K.
                                                                                                                                                                                                                                                                                                                                      AU096979.1 GI:8859661
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Mational Institute of Agrobiological Resources
Rice Genome Research Program, Kannondal 2-1-2, Tsukuba, Ibaraki
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                         (bases 1 to 297
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l: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
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81-298-38-7468
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/note="Green shoot (8 days old)"
79 c 68 g 57 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="S16022"
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Pred. No. 41;
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8 ACCTACGTAGCAGAAAGTTTTTACUUUCUGCUACGTAGGUUGGAAGGG 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anderson, O.A., Appels, R., Bailey, P., Blake, T., Close, T., Cloutier, S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A., Gustafson, P., Herrmann, R., Graner, A., Gustafson, P., Langridge, P., Lazo, G.R., Lin, J.J., McGuire, P., Ogihara, Y., Pecchioni, N., Qualset, C., Schuch, W., Selvaraj, G., Shariflou, M., Sorrells, M., Warburton, M. and Wenzel, G. International Triticeae EST Cooperative (ITEC): Production of
                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://wheat.pw.usda.gov/genome.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Key Lab. of Crop Germplasm & Biotechnology
Inst. of Crop Germplasm Resources
Beijing 100081 pr CHINA
Tel: 86 1 62186623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Jia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Expressed Sequence Tags for Species of the Triticeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              International Triticeae EST Cooperative (ITEC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CNW0ZEL010 ITEC CNW Wheat Powdery Mildew Resistant Library Triticum centrum cDNA clone CNW0ZEL010, mRNA sequence.
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                                                                                Conservative
                                                                                                                                                                                                                                                    84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               jizeng@mimi.cnc.ac.cn
                                                                                                                                                                                                                               /note="Vector: Lambda Triplex; Site_1: Sfil; Primer used:
5'-TCCGAGATCTGGACGAGC-3' 500 bp average insert size."
81 c 87 g 48 t
                                                                                                                                                                                                                                                                                                                                                   strain"
                                                                                                                                                                                                                                                                                                                                                      /dev_stage="seedling, challenged with powdery mildew
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="ITEC CNW Wheat Powdery Mildew Resistant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Triticum aestivum"
/cultivar="Powdery Mildew Resistant line"
/db_xref="taxon:4565"
/clone="CNW02EL010"
                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="leaf"
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/note="Green shoot (8 days old)"
84 c 72 g 56 t
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1. .297
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/db_xref="taxon:39947"
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                                                                                                        37.6%;
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                                                                                                            Score 25.6; DB 10;
Pred. No. 41;
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AU070730 Rice cDNA from young root Oryza sativa (japonica cultivar-group) cDNA clone R10161_2A, mRNA sequence.
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Oryza sativa (japonica cultivar-group)
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  305-8602, Japan
Tel: 81-298-38-7441
Fax: 81-298-38-7468
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AU057142 Oryza sativa mature leaf Nipponbare Oryza sativa (japonica cultivar-group) cDNA clone S21188_1A, mRNA sequence.
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                                                                                                                                                                                                                     Oryza sativa (japonica cultivar-group).
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                       EST
                                                                                                           Unpublished (1999)
Contact: Takuji Sasaki
                                                                                                                                                                                                                                                                                                                       AU057142.1 GI:4716026
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                 305-8602, Japan
Tel: 81-298-38-7441
Fax: 81-298-38-7468
                                                                   Rice Genome Research Program, Kannondai 2-1-2, Tsukuba,
                                                                                                                                                                     1 (bases 1 to 352)
Yamamoto, K. and Sasaki, T.
                                                                                                                                                                                                         Ehrhartoideae; Oryzeae; Oryza.
                                                                                         National Institute of Agrobiological Resources
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                                                                                                                                                 cDNA from mature leaf
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tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Takuji Sasaki
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98 c 96 g 97
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/db_xref="taxon:39947"
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Job time : 2409.76
                Search completed: March 17,
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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AU162789 Rice mature leaf Oryza sativa (japonica cultivar-group)
cDNA clone S21904, mRNA sequence.
AU162789
                                                                                                                                29;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Takuji Sasaki
National Institute of Agrobiological Resources
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sasaki, T. and Yamamoto, K.
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                                                                                                                                                                                                                                                                                                                                                                                  305-8602, Japan
Tel: 81-298-38-7441
Fax: 81-298-38-7468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rice cDNA from mature leaf (2000)
                                                                                                                                                 Similarity
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/clone_lib="Oryza sativa mature leaf Nipponbare"
/tissue_type="mature leaf"
y7 c 100 g 58 t
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/cultivar="Nipponbare"
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/tissue_type="mature leaf"
99 c 99 g 58 t
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/clone="S21904"
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Maximum DB seq length: 2000000000
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Maximum Match 100%
Listing first 45 summaries
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

	AUTHORS	REFERENCE			ORGANISM	SOURCE	SEGMENT	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	MMHIF1AS04	RESULT 1	
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MMHIFIASO4

MUS musculus hypoxia-inducible factor 1 alpha (Hifla) gene, exon 4.

AF004144.1 GI:2197137

4 of 15

Mus musculus.

Mus musculus.

Mus musculus.

Mus musculus.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Musinae; Mus.

1 (bases 1 to 85)

Luo,G., Guy.Z., Jain,S., Chan,W.K., Carr,K.M., Hogenesch,J.B. and
Bradfield,C.A.

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KEYWORDS
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                                                                                                                                                                                                                                                                         Submitted (24-FBB-1998) Departments of Pediatrics and Medicine, Institute of Genetic Medicine, Johns Hopkins University School of Medicine, 600 N. Wolfe St. Baltimore, MD 21287-3914, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             noHIFIAU3 538 bp DNA linear PRI 26-OCT-1998 Homo sapiens hypoxia-inducible factor 1 alpha subunit (HIF1A) gene, exons 3 and 4.
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Genomics 52 (2), 159-165 (1998)
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The human hypoxia-inducible factor lalpha gene: HIF1A structure and
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                                                                                                                                                                                           /map="14q21-q24"
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AX481424
Sequence
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Sequence 3 from Patent W00212326
AX451938
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                  38 from Patent W002055693
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EPDALTILLAPAAGDTIISLDFGSNDTETDDQQLEEVPLYNDVMLPSPNEKLQNTNLAM
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/gene="HIF1A"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (11-SEP-2000) Department of Neurosurgery, Affiliated Hospital of Xuzhou Medical College, Huaihai West Road, Xuzhou, Jiangsu 221002, China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sun, B., Zhao, H.R.,
Direct Submission
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1 (bases 1 to 2509)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                           / CLEANS LATION - MEGAGGANDKKKISSERRKEKSRDAARSRRSKESEVEYELAHOL
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LTDDGDMIY ISDNYNKYMGLTQFELTGELSYEDPTHPCDHEEMERUTHRINGLYKKGKE
ONTORSEFLAMKCTLTSERSGRTMNIKSATWKLLHCTGHIHVYDTNSNOPQCGYKKPEMT
CLYVLICEPIPHPSNIEIPLDSKTFLSRHSLDMKFSYCDERITELMGYEPEELLGRSIY
EYYHALDSDHLTKTHHDMETKGQYTTGQYRMLAKRGYVMYETGATVIYNTKNSQPQC
IVCVNYVYSGITQHDLIFSLAOTECVLKPVESSDMKTGLFTKVESBDTSSLFDKLKK
SPLDTABTTPKPLRSSADPALNQEVALKLEPNPESLELSFTMPQIQDTDSPSDSGSTRQ
SSPEPNSPSYCFYVDSDMVNEFKLELVEKLFAEDTEAKNPESTOOTDLLDLEMLAPYI
SSPENGSTRG
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SHPRSPNVLSVALSQRTTVPEEELNPKILALQNAQRKRKMEHDGSLFQAVGIGTLLQQ
                       PMDDDFQLRSFDQLSPLESSSASPESASPQSTVTVFQQTQTQEPTANATTTTATTDEL
KTVTKDRMEDIKILIASPSPTHIHKETTSATSSPYRDTQSRTASPNRAGKGVIEQTEK
                                                                                                                                                                                                                                                                                              /product="hypoxia-inducible factor 1 alpha subunit"
/protein_id="AAG43026.1"
/db_xref="GI:11995455"
                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                   /gene-"HIF1A"
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1. .2509
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512 c 500 g
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HIFla sequence in the Quechua, a high altitude population
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Homo sapiens hypoxia-inducible factor 1 alpha (HIF1A) gene,
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IVCVWYVVSGIIQHDLIFSLQQTECVLKPVESSDMKMTQLFTKVESEDTSSLFDKLKK
EPDALTILAPAAGDTIISLDGSNDTETDDQQLEEVPLYNDVHLSGPNEKLQNINLAM
SPLPTAETTKPLASSADPALNOEVALKLEPNPSSLEISFTMOQIODOTPSPBOGSTRQ
SSPEPNSPSEYCFYVDSDMVNEFKLELVEKLFAEDTEAKNPFSTQDTDLDLEMLAPY
PMDDFQLRSFDQLSPLSSSASPESASPQSTVTVFQQTQIQEPTANATTTTATTDEL
KTYTKDRNEDIKILASSPFHHHKETTSATSEYNDTOSRTASPNRAGKGVIEQTEK
SHPRSPNVLSVALSQRTTVPEEELNFKILALQNAQRKRKMEHDGSLFQAVGIGTLQQ
PDDHAATTSLSWKRVKGCKSSEQNGMEDKTILALQNAQRKRKMEHDGSLFQAVGIGTLQQ
PDDHAATTSLSWKRVKGCKSSEQNGMEDKTILIPSDLACRLLGQSMDESGLPQLTSY
                             DCEVNAPIQGSRNLLQGEELLRALDQVN"
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QNTQRSFFLRHKCTLTSRGRTMNIKSATWKVLHCTGHIHVYDTNSNQPQCGYKKPPMT
CLVLICEPIPHPSNIEIPLDSKTFLSRHSLDMKFSYCDERITELMGYEPBELLGRSIY
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/product="hyparia-inducible factor 1 alpha"
/protein_id="happaria-inducible factor 1 alpha"
/protein_id="happar
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/chromosome="14"
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/cell_type="lymphoblast"
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Query Match

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DB 9;

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Sequence 2 from Patent WO0162965.
AX230580
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Location/Qualifiers
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HOMO Sapiens cell-line GM11201 hypoxia-inducible factor 1 alpha
(HIFIA) mRNA, complete cds.
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                                                                                                                                                                                    Submitted (18-NOV-1999) Zoology, University of British Columbia, 6270 University Blvd., Vancouver, BC V6T 1Z4, Canada
                                                                                                                                                                                                                                                                              HIF1a sequence in the Quechua, a high altitude population
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/db_xref="taxon:9606"
528 c 513 g 648
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/note="HIF1-alpha"
                                            /ceil_line="GM11201 (Ccriell)"
/cell_type="lymphoblast"
/note="derived from a high altitude native (Quechua)"
                                                                                            /map="14g21-g24"
                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
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(HIF1A) mRNA, complete cds.
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QNTQRSFFLRMKCTLTSRGRTMNIKSATWKULHCTGHHHYDTMSNOPOCGYKKPMT
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IVCVNYVSGIIQHDLIFSLQQTECVLKPVBSSDMKWFGLFTKKESEDTSSLEDKKKK
EPDALTTLAPAAGDTIISLDFGSNDTETDDOQLEEVPLYNDVMLPSPNEKLQNINLAM
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KTYTKDRMEDIKILLASPSPTHHHKETTSATSSPYRTYOSKTASSPNRAGKGVIEGTEK
SHPRSPNYLSVALGQTTVPEEEELNPKILALQNAQRKRKMEHDGSLFQAVGIGTLAQ
SPDHAATTSLSWKRVKGCKSSEQNGMEGKTILALQNAQRKRKMEHDGSLFQAVGIGTLAQ
PDDHAATTSLSWKRVKGCKSSEQNGMEGKTILLIPSDLACRLLGGSMDESGLPQLTSY
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/db_xref="G1:6636317"
/translation="MEGAGGANDKKKISSERRKEKSRDAARSRRSKESEVFYELAHQL
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                                                                                                                                                                                                                                                                       /map="14q21-q24"
/cell_line="GM11197 (Coriell)"
/product="hypoxia-inducible factor 1 alpha"
/protein_id="AAF20140.1"
                                                                                                                                                                                                                           /cell_type="lymphoblast"
/note="derived from a high altitude native (Quechua)"
                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                 /note="transcription factor; hypoxia-inducible factor la"
/codon_start=1
                                                                                               /gene="HIF1A"
                                                                                                                                                /note="HIF1-alpha"
                                                                                                                                                                          /gene="HIF1A"
                                                                                                                                                                                                                                                                                                                     /chromosome="14"
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                                                                                                                                                                                             D-37073 Goettingen, PRG
On Mar 4, 1998 this sequence version replaced gi:2632130.
Location/Qualifiers
                                                                                                                                                                                                                                                               Direct Submission
Submitted (27-FEB-1998) T. Kietzmann, Inst.
Cell Biol., Georg-August-Univ. Goettingen, F
                                                                                                                                                                                                                                                                                                                                                                   D-37073 Goettingen, FRG
Revised by [3]
3 (bases 1 to 2711)
                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (18-NOV-1995) T. Kietzmann, Inst. Of Biochem. /
Cell Biol., Georg-August-Univ. Goettingen, Humboldtallee
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                                                                                                                                                                                                                                                                                                                                                    Kietzmann,T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kietzmann,T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Perivenous expression of the mRNA of the three hypoxia-inducible factor alpha-subunits, HIFlalpha, HIF2alpha and HIF3alpha, in rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kietzmann, T., Cornesse, Y., Brechtel, K., Modaressi, S. and Jungermann, K.
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DCEVNAPIOGSERNLLQGEELLRALDQVN*
1 526 c 507 g 666 t
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CLVLLCEPIPHPSNIEIPLDSKTFLSHHSLDMKFSYCDERITELMGYEPEELLGRSIY
EYYHALDSDHLTXTHHDMFTKGQVTTGGYRMLAKRGYLWYETGATVIYMTKNSQPQC
EYVNYVYSGIIQHDLIFSLQQTECVLKPVESSDMKMTQLYKKVESEDTSSLFDKKK
EPDALTLLAPAAGDTIISLDFCSNDTETDDQQLEEVPLYNDVMLPSPNEKLQNINLAM
SPLPTAETPKPLRSSADPALNQEVALKLEPNPESLELSFTMPQIQQTPSPSDGSTRQ
SSPEPNSPSEYCFYVDSDMVNEFKLELVEKLFAEDTEAKNPFSTQDTDLDLEMLAPYI
                                      /cell_line="primary hepatocytes"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PMDDDFQLRSFDQLSFLESSSASPESASPQSTVTVFQQTQIQEPTANATTTATTDEL
KTVTKDRMEDIKILIASPSPTHIHKETTSATSSPYRDTQSRTASPNRAGKGVIEQTEK
SHPRSPNVLSVALSQRTTVPEEELNPKILALQNAQRKRKMEHDGSLFQAVGIGTLLQQ
/codon_start-1
                                                                                                             /db_xref="taxon:10116"
                                                                                                                                        /organism-"Rattus norvegicus"
/strain-"Wistar"
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PLPHNVSSHLDKASVMRLTISYLRVRKLLDAGDLDIEDDMKAQMNCFYLKALDGFVMV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 3551)
Tanaka, S. and Sugimachi, K.
Direct Submission
Submitted (20-0CT-2001) Shinji Tanaka, Kyushu University, Graduate School of Medical Sciences, Department of Surgery and Science; 3-1-1 Maidashi, Fukuoka, Fukuoka 812-8582, Japan (E-mail:shinjit@surg2.med.kyushu-u.ac.jp, Tel:81-92-642-5466,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tanaka, S. and Sugimachi, K.
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Homo sapiens HIF1A mRNA for hypoxia-inducible
                                                                                                                                                                                                                                                                                                                                                                                                                                        Fax:81-92-642-5482
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AB073325.1 GI:16326343
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AB073325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypoxia-inducible factor-1 alpha variant isolated from human liver
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GDRAPTMSLSWKRVKGYISSEQDGMEQKTIFLIPSDLACRLLGQSMDESGLPQLTSYD
CEVNAPIQGSRNLLQGEELLRALDQVN"
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IVCVNYVSGIIQHDLIFSLQGDTESVLKPVESSDKWTQLFTKVESSDFSCLFDKLKK
EPDALTLAPAAGDTIISLSDFSCDFFETEDQGLEDVPLYNDVMFPSSNEKLNINLANS
PLPASSTPKPLRSSADPALNQEVALKLESSPESLGLSFTMPQIQQPASPSDGSTRQS
PLPASSTPKPLRSSADPALNQEVALKLESSPESLGLSFTMPQIQQPASPSDGSTRQS
PEPNSEYCCDVDSDMYNVFKLELVEKLFAEDTEAKNPFSAQDTDLDLEMLAPYIDIB
MDDDFQLRSPDQLSPLESNSPSPSVGTVTGFQQTQLOKPTITVTAATTATTTDIS
MDDDFQLRSPDQLSPLESNSPSPSTQVPQEMTTAKASAYSGTHSRTASPDRAGKRVIEKTDK
KAVTKDNIEDIKILLASPPSTQVPQEMTTAKASAYSGTHSRTASPDRAGKRVIEKTDK
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                                                                 /product="hypoxia-inducible factor 1 alpha variant"
/protein_id="BAB70608.1"
/db_xref="GI:16326344"
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QNTQRSFFLRMKCTLTSRGRTMNIKSATWKVLHCTGHIHVYDTSSNQPQCGYKKPPMT
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PLPHNVSSHLDKASVMRLTISYLRVRKLLDAGDLDIEDEMKAQMNCFYLKAPDGFYMV
LTDDGDMIYISDNVNKYMGLTQFELTGHSVFDFTHPCDHEEMREMLTHRNGLVKKGKE
                                                                                                                                                        /codon_start=1
                                                                                                                                                                          /note="HIF-1 alpha variant"
                                                                                                                                                                                                       /gene="HIF1A"
                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
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/protein_id="CAA70701.1"
/db_xref="GI:2632131"
                                                                                                                                                                                                                                                      /gene="HIF1A"
                                                                                                                                                                                                                                                                                                     tissue_type="liver"
                                                                                                                                                                                                                                                                                                                                                                                                      ocation/Qualifiers
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Pred. No. 0.
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U22431.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (09-MAR-1995) Gregg L. Semenza, Genetics, The Johns Hopkins University Sc. Wolfe St., Baltimore, MD 21287-3914, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wang, G.L., Jiang, B.H., Rue, E.A. and Semenza, G.L.
Hypoxia-inducible factor 1 is a basic-helix-loop-helix-PAS
heterodimer regulated by cellular O2 tension
Proc. Natl. Acad. Sci. U.S.A. 92 (12), 5510-5514 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wang,G.L., Jiang,B.-H., Rue,E.A. and Semenza,G.L. Direct Submission
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CLVLICEPIPHPSNIEIPLDSKTFLSRHSLDMKFSYCDERITELMGYEPEELLGRSIY
EXYHALDSDHLTWTHHDMFTKGCVTTGOYRMLAKRGGYWWETGDYINTKNSQPQC
IVCVNYVVSGIIQHDLIFSLQOTECVLKPVESSDMKMTQLFTKVESEDTSISLIPKLKK
EPDALTILAPAAGDTIISLDFGSNDTETDDQQLEEVPLYNDVMLPSPNEKLQNINLAM
SPLPTAETFKPLRSSADPALNQEVALKLEPNPESLELSFTMPQIQDGPSPSDGSTRQ
                                                                                                            PMDDDFQLRSFDQLSPLESSSAS PESASPQSTYTVFQQTQIQEPTANATTTATTDEL
KTVTKDRMEDIKILIASPSPTHIHKETTSATSSPYRDTQSRTASPNRAGKGVIEQTEK
SHPRSPNVLSVALSQRTTVPEEELNPKILALQNAQRKKKMEHDGSLFQAVGII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EYYHALDSDHLTKTHHDMFTKGQVTTGQYRMLAKRGGYVWVETQATVIINTKNSQPQC
IVCVNYVVSGIIQHDLIFSLQQTECVLKPVESSDMKMTQLFTKYUSSEDTSSLFDKLKK
EPDALTILAPAAGDTIISLDFGS NDTETDDQQLEEVPLYNDVMLPSPNEKLQNINLAN
SPLPTAETPKPLRSSADPALNQEVALKLEPNPESLELSTMPQIQQTPSPSDGSTRQ
SSPEDNSGPSEYCFYUSDMVNEFKLELYEKLFAEDTEAKNPFSTQDTDLDLEMLAPII
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CLVLICEPIPHPSNIEIPLDSKTFLSRHSLDMKFSYCDERITELMGYEPEELLGRSIY
                                                                                                                                                                                                                                                                                                                                                          /gene="HIF-1 alpha"
29. .2509
                                                                                                                                                                                                                                                                       /codon_start=1
                                                                                                                                                                                                                                                                                         /standard_name="hypoxia-inducible factor 1,
/note="basic helix-loop-helix transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (04-APR-1998) Departments of Physiology and Pharmacology, Medical College of Wisconsin, 8701 Watertown Plank Road, Milwaukee, WI 53226, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 3718)
20u,A.P., Yang,Z.Z., Li,P.L. and Cowley AW,J.R.
0xygen-dependent expression of hypoxia-inducible factor-lalpha in
renal medullary cells of rats
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AF057308
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                                                                                         PMDDDFQLRSFDQLSPLESSSASPESASPQSTVTVFQQTQIOEPTANATTTTATDEL
KTVTKUMEDIKILASPSPTHIHKETTSATSSPXTDTQSSTASPNRAGKVIEQTEK
SHPRSPNLLSVALSQRTTVPEEELNFKILALQNAQKKRKMEHDGSLFQAVGIGTTLQQ
PDDHAATTSLSWKRVKGCKSSEQNGMEQKTIILIPSDLACRLLGQSMDESGLPQLTSY
                    CIVCVNYVVSGIIQHDLIFSLQQTESVLKPVESSDMKMTQLFTKVESEDTSCLFDKLK
KEPDALTLLAPAAGDTIISLDFGSDDTETEDQQLEDVPLYNDVMFPSSNEKLNINLAM
SPLPASETPKPLRSSADPALNQEVALKLESSPESLGLSFTMPQIQDQPASPSDGSTRQ
                                                                                                                                                                                          /codon_start=1
/product=hypoxia-inducible factor-1 alpha"
/protein_id="AAD24413.1"
/db_xref="GI:4580533"
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SSPEPNSPSEYCFDVDSDMVNVFKLELVEKLFAEDTEAKNPFSAQDTDLDLEMLAPYI
                                                                           YEYYHALDSDHLTKTHHDMFTKGQVTTGQYRMLAKRGGYVWVETQATVIYNTKNSQPQ
                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Rattus norvegicus"
/strain="Sprague Dawley"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                        /note="transcription factor; RH1F-1"
                                                                                                                                                                                                                                                                                          /gene="Hifla"
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                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="kidney"
/dev_stage="adult"
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                                                                 Wenger,R.H., Roifs,A., Marti,H.H., Guenet,J.L. and Gassmann,M. Nucleotide sequence, chromosomal assignment and mRNA expression of mouse hypoxia-inducible factor-1 alpha Biochem. Blophys. Res. Commun. 223 (1), 54-59 (1996)
                                                                                                        Direct Submission
Submitted (07-FEB-1996) R.H. Wenger, Institute of Physiology, University of Zuerich-Irchel, Winterthurerstrasse 190, CH-8057 Zuerich, SWITZERLAND
                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 3746)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24;
                                                                                                                                                                                      Wenger, R.H.
                                                                                                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                                                                                             HIF-lalpha; hypoxia-inducible factor one alpha.
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M.musculus mrna for hypoxia-inducible factor I alpha.
x95580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Method for examining ischemic conditions
Patent: WO 018818-A 759 22-NOV-2001;
School Juridical Person Nihon University (JP)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ishikawa, K., Asai, S., Takahashi, Y., Nagata, T. and Ishii, Y.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Sequence 759 from Patent WOO188188.
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YTXDNIEDIKILIASPPSTQVPQEMTTAKASAYSGTHSRTASPDRAGKRVIEKTDKAH
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VNAPIQGSRNLLQGEELLRALDQVN*
1733 c 762 g 1098 t
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Job time :

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501 CCATGTGACCATGAGGAAATGAGAG 525

Search completed: March 17, 2003, 11:24:12

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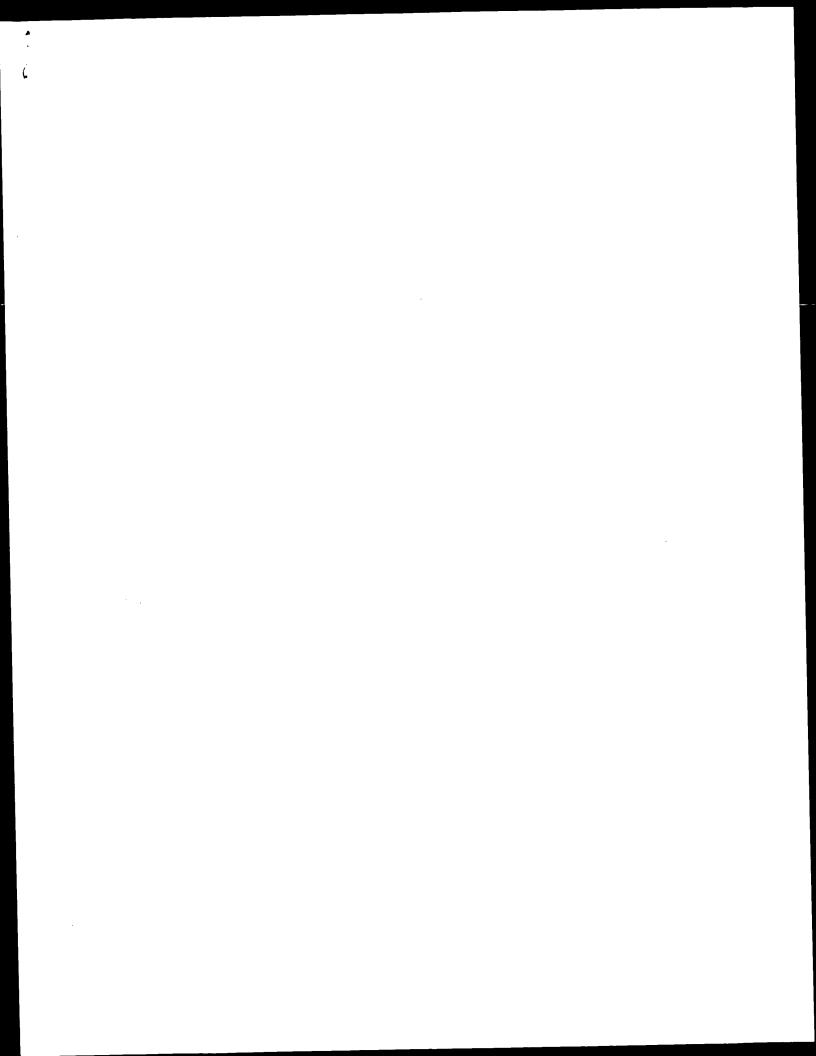
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

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ABK11552
ID ABK11552;
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AC ABK11552;
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DT 05-JUN-2002 (first entry)
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DT 05-JUN-2002 (first entry)
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DE Human cDNA encoding hypoxia-inducible factor-1;
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XX
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Human cDNA encoding hypoxia-inducible factor-1 alpha, HIF-1.
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DE Human cDNA encoding hypoxia-inducible factor-1 alpha, HIF-1.
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DE Human cDNA encoding hypoxia-inducible factor-1 alpha, HIF-1.
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DE Human cDNA encoding hypoxia-inducible factor-1 alpha, HIF-1.
XX

DE Human cDNA encoding hypoxia-inducible factor-1 alpha, HIF-1.
XX

DE Human cDNA encoding hypoxia-inducible factor-1 alpha, HIF-1.
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DE Human cDNA encoding hypoxia-inducible factor-1;
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DE Human cDNA encoding hypoxia-inducible factor-1;
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DE Human cDNA encoding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modulates N-TAD function and antagonists, agonists, modulators and HIF-1 peptide fragments useful for modulating HIF-1 function or the function of proteins that interact with it. The isolated polypeptides and their fragments with altered residues are useful in methods for treating diseases. The disease is an ischaemic condition, e.g. brain infarction, heart infarction or circulatory disorder. The disease may also be cancer, heart infarction, demyelinating disorders, diffuse proliferative plomerulonephritis, toxoplasmosis caused retinochorioiditis HIV (human immunodeficiency virus) caused Tat anglogenesis, HIV-caused Kaposi's sarcoma, hepatitis-caused inflammation, hepatitis-caused anglogenesis, sarcoma, hepatitis-caused inflammation, hepatitis-caused anglogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a polypeptide comprising hypoxia-inducible factor-1 (HIF-1) with alterations of the transactivation domain (N-TAD of C-TAD). Also included are nucleic acids encoding the altered proteins, a vector comprising the nucleic acid, a host cell transformed with the vector, methods for producing the protein or its functional fragment or an isolated degradation box, a method of screening for an agent that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polypeptides comprising hypoxia-inducible factor-1 with alterations of the transactivation domain, useful treating ischaemic conditions, e.g. brain infarction, heart infarction or circulatory disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chronic ulceration, proliferative retinopathy, retina haemangioblastomas, neovascularisation, arterial hypervascularisation, sarcoidosis, bullous skin disease, vasculitis with angiogenesis, dermatomyositis with angiogenesis, dermatomyositis with surfunction arthritis, juvenile osteoarthritis, polyarthritis, aneurysm or atheroma. The present sequence encodes HIF-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 73-76; 80pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; HIV; HCV; gene expression; oligoribonucleotide; tumour; pathogen; plasmodium; virus; viroid; cytokine; prion; antisense oligonucleotide; cytostatic; virucide; protozoacide; antibacterial; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ASPE-) ASPERA PHARM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2481 BP; 829 A; 512 C; 500 G; 640 T; 0 other;
                                                                                                                                                                                                                                                                                                    DE10100586-C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human polynucleotide SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABL91695 standard; DNA; 2481
                                                                                                                                                    09-JAN-2001; 2001DE-1000586
                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
       (RIBO-) RIBOPHARMA AG
                                                                            09-JAN-2001; 2001DE-1000586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 412 CCATGTGACCATGAGGAAATGAGAG 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CCATGTGACCATTAGGAAATGAGAG 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93.6%;
96.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 23.4; DB 24; Length 2481;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38
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Дb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                by introducing double-stranded complementary oligoRNA having unpaired
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Differential expression; polymorphism; biological pathway; IRES; GFP; ss; internal ribosome entry site; green fluorescent protein; HIF-1 alpha; hypoxia inducible factor 1 alpha; hypoxia regulated gene; macrophage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human HIF-1 alpha DNA used in identification of hypoxia regulated genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2481 BP; 829 A; 512 C; 500 G; 640 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          terminal bases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAS14154 standard;
                                                                                                                                                                                                                                                                                                                              22-FEB-2001; 2001WO-GB00758
                                                                                                                                                                                                                                                                                                                                                                            30-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                           WO200162965-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                               Kingsman AJ;
                                                                                                                                                                                                           (OXFO-) OXFORD
                                                                                                                                                                                                                                                            28-JUL-2000;
                                                                                                                                                                                                                                                                                  22-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                412 CCATGTGACCATGAGGAAATGAGAG 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CCATGTGACCATTAGGAAATGAGAG 25
                                                                                                                   2001-589807/66.
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2000GB-0018679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                             BIOMEDICA UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cells, useful for e.g. treating tumors,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.19;
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Screening a genetic element involved in a cellular process, comprises comparing gene expressions in a cell, and a second cell that has altered levels of genes used in the process, and detecting an element little control of the cont

varied expression

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Best Local S
Matches 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 whose expression differs, by comparing expression under different environmental conditions. The method is useful for identifying mutations and polymorphisms that affect the biological response to a particular cellular process. The method also allows the molecular dissection of biological pathways by altering a particular pathway under study. By introducing a heterologous nucleic acid into a cell population, the level of a particular molecule can be influenced, allowing a pathway to be dissected into its precise molecular components. The main use of the method is to compare gene expression in cells from a diseased patient of the method is to compare gene expression in cells from a diseased patient and from a normal patient. This sequence represents a human hypoxia inducible factor 1 alpha (HIF-1 alpha) which is inserted into an Adapt ires-GFP plasmid for use in identification of hypoxia-regulated genes in
                                                                                                                                                                                                                                                                                                                       CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid sequence of human hypoxia inducible factor 1 alpha.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to differential expression screening to identify genetic element involved in a cellular process. The method involves comparing gene expressions in two cells, where one cell has altered levels of a biological molecule, and identifying the genetic element
            Regulation of trophoblast invasion - by, e. (factor-beta3 inhibitor, useful for detecting
                                                                                                                                                                          07-MAR-1997;
                                                                                                                                                                                                     05-MAR-1998;
                                                                                                                                                                                                                                  17-SEP-1998
                                                                                                                                                                                                                                                               WO9840747-A1
                                                                                                                                                                                                                                                                                                                                                                 Homo
                                                                                                                                                                                                                                                                                                                                                                                            preeclempsia;
                                                                                                                                                                                                                                                                                                                                                                                                          trophoblast invasion regulation; inhibitor; HIF-1 alpha; TGF-beta family cytokine receptor; hypoxia inducible factor 1 alpha.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2; Page 96-97; 103pp; English.
preeclempsia in pregnant women
                                                          P-PSDB; AAW80418.
                                                                                                                              (HOSP-) HOSPITAL FOR SICK CHILDREN (MOUN) MOUNT SINAI HOSPITAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               439
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                                                                      1998-520837/44.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        transforming
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                                                                                                   Lye
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                                                                                                                                                                                                                                                                                                                                                                                            pregnanancy; choriocarcinoma; ss.
                                                                                                                                                                         97US-0039919
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                                                                                                                                                                                                                                                                                        /#tag= a
/product= HIF-1 alpha
                                                                                                                                                                                                                                                                                                         /*tag=
                                                                                                                                                                                                                                                                                                                                   ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               839
                                                                                                                                                                                                                                                                                                                                                                                                                                  growth factor-beta 3; TGF-beta3; oxygen tension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93.6%;
                                                                                                   Post
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Pred. No. 0
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).19;
                           e.g. transforming
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               treating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to identify a
                           growth
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RESULT 5
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Best Local
risk of developing a haematol (MDR). The method involves ac (HIF-1) binding molecules or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human: haematologic malignancy; multidrug resistance; MDR; SUMO-1; hypoxia inducible factor 1; small ubiquitin-like-modifier; HIF-1; lymphoid disorder; chronic lymphoproliferative disorder; lymphoma; myeloid disorder; lymphocytic leukaemia; thrombocythaemia; myeloma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence encodes human hypoxia inducible factor 1 alpha (HIF-1 alpha). The specification describes a composition for regulating trophoblast invasion which comprises an inhibitor of transforming growth factor-beta 3 (TGF-beta3), TGF-beta family cytokine receptors, HIF-1 alpha or oxygen tension. The composition is used in methods of diagnosing, monitoring, preventing or treating conditions requiring regulation of trophoblast invasion, especially preeclempsia in pregnant
                                                                                                                  Treating a subject (at risk of) having a hematologic malignancy or multidrug resistance, e.g. lymphoma or myeloma, by administering hypoxia inducible factor 1 binding molecules or small
 The invention relates to a method of treating a subject having or at risk of developing a haematologic malignancy or multidrug resistance (MDR). The method involves administering hypoxia inducible factor-1 (HIF-1) binding molecules or small ubiquitin-like-modifier (SUMO)-1
                                                                          Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human HIF-lalpha cDNA.
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                                                                                                     ubiquitin-like-modifier-1 binding molecules
                                                                                                                                                                                                                                                     (BGHM ) BRIGHAM & WOMENS HOSPITAL
                                                                                                                                                                                                                                                                                                                25-OCT-2001; 2001WO-US49856
                                                                                                                                                                                                                                                                                                                                             02-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                           WO200234291-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polycythaemia vera; hypoxia responsive element; HRE; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            angiogenic myeloid metaplasia; myeloid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3678 BP; 1197 A; 695 C; 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              women or choriocarcinomas.
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                                                                                                                                                                                2002-471427/50.
)B; AAE24212.
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96.0%;
                                                                          92pp;
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The invention relates to detecting (M1) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (Gs) identified DNA chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated GC, where differential expression of Gs is indicative of GCA. Also included are modulating (M2) GA by contacting GC with an agent that alters the expression of at least one gene in Gs; (2) screening that alters the expression of at least one gene in Gs; (2) screening that alters the expression of at least one gene in Gs; (2) screening (M2) GA by contacting GC with an agent capable of modulating GCA or an inflammatic.
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                                                                                                                                                                                                                                                                                                                                                                                                                 Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasis; rheumatoid arthritis; glomerulonephritis; asthma; thrombosis; cardiac reperfusion injury; renal reperfusion injury; ARDS;
                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID No 838; 114pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-435328/46.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      granulocyte activation; chronic inflammation; allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Crohn's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; ss; granulocytic cell; DNA chip; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      respiratory distress syndrome; inflammatory bowel disease, 's disease; ulcerative colitis; periodontal disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA differentially expressed in granulocytic cells #838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENE LOGIC INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3678 BP; 1197 A; 695 C; 675 G; 1111 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the gene expression profile; (3) detecting (M4) an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease (e.g. psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, reperfusion injury, ARDS, adult respiratory distress syndrome,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modulating GA; M3 is useful for screening an agent capable of modulating GCA preferably in an inflammation in a tissue; M4 is useful for detecting an inflammation (especially chronic) in a tissue, an allergic
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                                                                                            06-JUN-1995;
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    (UYJO ) UNIV JOHNS HOPKINS SCHOOL MED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   factor-1 alpha; HIF-1; tissue damage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Þ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kozak sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23.4;
No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DΒ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           granulocytes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for
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RESULT 8
AAZ99537
ID AAZ9
XX AAZ9
XX DNA
XX DNA
XX Huma
KW Huma
KW 1sch
XX 1sch
XX Homo
XX Homo
CS Homo
CS Homo
CS Homo
CS HOM
C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human hypoxia inducible factor-1 (HIF-1), a DNA binding protein that binds to the enhancer region of e.g. erythropoietin and vascular endothelial growth factor (VEGF) genes. The DNA sequence is a composite of 3 clones obtd. by screening an Hep3B library and by database analysis. HIF-1 alpha nucleic acids can be used to prepare recombinant HIF-1 alpha in transformed host cells, as probes, and in the gene thorapy of HIF-1-mediated or hypoxia-related disorders such as atherosclerotic coronary or cerebral artery disease; antisense sequences inhibit HIF-1 expression e.g. to treat
                                                              WPI; 2000-246493/21.
P-PSDB; AAY69407.
                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200010578-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human: hypoxia-inducible factor 1 alpha: HIF-lalpha; variant; hypoxia inducible gene; hypoxia inducible factor; hypoxia; ischemia related damage; angiogenesis; coronary artery disease; ischemic tissue damage; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA encoding a wild type human hypoxia inducible factor-1 alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding human hypoxia-inducible factor enhancing expression of structural gene and
Variant forms of hypoxia-inducible factor (HIF)-1 alpha, useful
                                                                                                                                                                                                                                                                25-AUG-1998;
                                                                                                                                                                                                                                                                                                                      25-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                              02-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAZ99537 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3736 BP; 1255 A; 695 C; 675 G; 1111 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tumour proliferation mediated by VEGF-induced angiogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A DNA sequence (AAT45937) codes for the alpha subunit (AAW06557) of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypoxia-related tissue damage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      semenza
                                                                                                                                                                                                        (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CCATGTGACCATTAGGAAATGAGAG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCATGTGACCATGAGGAAATGAGAG 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1997-043061/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Page 49-53; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW06557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                98US-0148547
                                                                                                                                                                                                                                                                                                                      99WO-US19416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers 29..2509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= a
/product= "hypoxia inducible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 23.4;
Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DΒ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 alpha -
treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        factor-1 alpha"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
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RESULT 9
ABI99710
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             stable under hypoxic and non-hypoxic conditions. The variants comprise amino acid residues 1-391 and 521-826, 549-826, 576-826, 429-826, 469-826, 508-826, 508-826, 517-826 or 5
                conditions, comprising measuring the expression levels of particular genes (I) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (I). The method is useful for examining the ischaemic condition (e.g. compressive
                                                                                                                                                                                                                                                              Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABI99710 standard; cDNA; 3746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3736 BP; 1255 A; 695 C; 675 G; 1111 T; 0 other;
                                                                                                                               The present invention describes a method for examining ischaemic
                                                                                                                                                                                       Claim 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ishikawa K, Asai S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-MAY-2000; 2000JP-0145977.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-NOV-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vasospastic ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABI99710;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 80-89; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     treating hypoxia or ischemia-related tissue damage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  440 CCATGTGACCATGAGGAAATGAGAG 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CCATGTGACCATTAGGAAATGAGAG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          present sequence encodes a wild type human hypoxia-inducible factor present sequence encodes a wild type human hypoxia-inducible factor)-1 alpha variants that are
                                                                                                                                                                                                                                                                                                                                                                                                            2002-034733/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ischaemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24;
                                                                                                                                                                                                                                                                                                                                                                                  ABB57270
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                                                                                                                                                                                  Page 1863-1869; 2690pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001WO-JP04192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           condition related cDNA sequence SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Takahashi Y, Nagata T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ischaemic condition; ischaemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 23.4; D. Pred. No. 0.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ishii Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The variants comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ID NO:759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3736;
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ischaemia, occlusive ischaemia or vasospastic ischaemia) by

measuring

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RESULT 10
AAS61690
ID AAS611
XX AAS61
XX AAS61
XX AAS61
XX AAS61
XX AAS61
XX Lung
XX Human
KW Human
KW tumo
XX Homc
XX Tung
XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8888888888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-APR-2000;
21-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expression levels of particular genes (ABI99202 to ABI99912, encoding the protein sequences in ABB57027 by or by determining the expression profile of a gene group comprising these genes. The expression levels or expression profiles produced by these genes are used as an indicator when screening for ischaemic condition improving drugs or therapeutics for ischaemic diseases. ABI99913 and ABI99914 represent PCR primers for a mouse ischaemic condition related sequence,
                           determining cancer in a patient. (I), (II) or antigen-presenting cells expressing (II) is useful for stimulating and/or expanding T cells specific for a tumour protein. The method comprises contacting T cells with one of the components under conditions to permit the stimulation
                                                                                                                                                                                                                                  The invention relates to novel isolated lung small cell cancer antigen polynucleotides (I) and polypeptides (II) used in a method of detecting cancer in a patient. The method is optionally performed by utilising oligonucleotides (III), where the biological sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lung tumour polynucleotide and polypeptides useful in therapy diagnosis of cancer especially lung cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-SEP-2000;
14-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-APR-2001; 2001WO-US11859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; cytostatic; antitumour; lung small cell cancer antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3746 BP; 1124 A; 740 C; 740 G; 1142 T; 0 other;
                                                                                                                                                                             from the patient is contacted with (III), detecting the amount polynucleotide hybridised to (III) in the sample and comparing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200177168-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tumour; lung cancer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-JAN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAS61690 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                which are used in the exemplification of the present invention.
                                                                                                                                           amount of polynucleotide to a predetermined cut-off value and thereby
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAU69409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lung small cell carcinoma antigen, cDNA #231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                501
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expansion of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wang T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-196780P.
2000US-213361P.
2000US-229763P.
2000US-2330629P.
2000US-232565P.
2000US-257037P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001US-260796P
                                                                                                                                                                                                                                                                                                                                                                                          201-202;
the cells. A composition comprising (I) is useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mohamath
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96.0%;
                                                                                                                                                                                                                                                                                                                                                                                          295pp; English.
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Pred. No. 0
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                                                                                                                                                                                                                                                                                                   detecting
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      for
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AAX58980
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
      to amplify additional flanking sequences from a commercial HepG2 library. MOP1 is also known as hypoxia inducible factor 1 alpha. The factor is induced by low oxygen. It interacts with HSP90 and with ARNT. The ARNT-dimerised factor regulates expression of erythropoietin, among other genes. The invention also provides novel MOPS 2-9 nucleic acids (see AAX5981-88) and proteins (see AAY06289-97). These are useful in a variety of research, diagnostic and therapeutic applications. Several of the MOPS are alpha-class hypoxia-inducible factors. Others are involved in
                                                                                                                                                                          search of human ESTs designed to identify basic-helix-loop-helix-PAS (bHLH-PAS) proteins that interact with either the Ah receptor (AHR) or the Ah receptor nuclear translocator (ARNT). To obtain extended
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    stimulating an immune response in a patient and for inhibiting the development of a cancer especially lung cancer in a patient. An isolated T cell population is useful for removing tumour cells from biological sample and for inhibiting the development of cancer in a patient. AAS61460-AAS61874 represent novel human lung small cell
                                                                                                                                                         or the Ah receptor nuclear translocator (ARNT). To obtain extended open reading frames for each EST, an anchored-PCR strategy was used
                                                                                                                                                                                                                        This is the nucleotide sequence of a cDNA encoding MOP1 (see AAYO6289), a member of the PAS superfamily, where PAS stands for PER/ARNT/SIM domains. The cDNA was identified in an iterative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cancer antigen coding sequences of the invention.
                                                                                                                                                                                                                                                                                                                        Developmental signal transduction associated proteins
                                                                                                                                                                                                                                                                                                                                                       P-PSDB; AAY06289
                                                                                                                                                                                                                                                                                                                                                                                                      Bradfield CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAX58980 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3927 BP; 1241 A; 782 C;
                                                                                                                                                                                                                                                                                          Example
                                                                                                                                                                                                                                                                                                                                                                                                                                      (WISC ) WISCONSIN ALUMNI RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOP1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            670 CCATGTGACCATGAGGAAATGAGAG
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                                                                                                                                                                                                                                                                                                                                                                         1999-371120/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               member of the PAS superfamily; bHLH-PAS; human;
cription regulator; hypoxia inducible factor 1 alpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transcription
                                                                                                                                                                                                                                                                                          1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                      Page 93-94; 106pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                      Gu YZ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97US-0066863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98WO-US25314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers 265..2745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              regulator MOP1 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93.6%;
96.0%;
                                                                                                                                                                                                                                                                                                                                                                                                    Hogenesch JB,
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Pred. No. 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           748 G; 1156 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3927;
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ARESULT 13
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                                                                                              The invention relates to isolated polynucleotide (I) and CD polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC polymerase and in recombinant production of (II). The complex comp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3933 BP; 1243 A; 784 C; 750 G; 1156 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding novel human diagnostic protein #20862.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAS85058 standard; cDNA; 4162 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; ABG20871.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC.
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23-AUG-2000; 2000US-0649167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-FEB-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                           ttp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        medical imaging; diagnostic; genetic disorder; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene mapping; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 23.4;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               forensic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3933;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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Sequence 4162 BP; 1286 A; 843 C; 813 G;

1220 T; 0 other;

Q

1 CCATGTGACCATTAGGAAATGAGAG 25 Conservative

Matches Query Match Best Local

Local Similarity

93.6%;

,.

Pred. No. Score 23.4; Mismatches

0.24; DB 22;

Indels Length 10355;

<u>,,</u>

Gaps

0

Sequence 10355 BP; 3060 A; 2212 C; 2373 G; 2710 T; 0 other;

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                            whose expression differs, by comparing expression under different environmental conditions. The method is useful for identifying mutations and polymorphisms that affect the biological response to a particular cellular process. The method also allows the molecular dissection of biological pathways by altering a particular pathway under study. By introducing a heterologous nucleic acid into a cell population, the level of a particular molecule can be influenced, allowing a pathway to be dissected into its precise molecular components. The main use of the method is to compare gene expression in cells from a diseased patient and from a normal patient. This sequence represents psMART CMV-HIF from a vector expressing hypoxia inducible factor 1 alpha (HIF-1 alpha) which is used in methods of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                   Screening a genetic element involved in a cellular process, comprises comparing gene expressions in a cell, and a second cell that has altered levels of genes used in the process, and detecting an element
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Differential expression; polymorphism; biological pathway; IRES; GFP; internal ribosome entry site; green fluorescent protein; HIF-1 alpha; hypoxia inducible factor 1 alpha; hypoxia regulated gene; macrophage;
                                                                                                                                                                                                                                                  The invention relates to differential expression screening to identify genetic element involved in a cellular process. The method involves comparing gene expressions in two cells, where one cell has altered levels of a biological molecule, and identifying the genetic element
                                                                                                                                                                                                                                                                                                                                                                                  with varied expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pSMART CMV-HIF DNA from a vector expressing HIF-1 alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAS14156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAS14156 standard; DNA; 10355 BP
                                                                                                                                                                                                                                                                                                                                              Example 5; Page 97-101; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-589807/66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kingsman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (OXFO-) OXFORD BIOMEDICA UK LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-FEB-2000;
28-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200162965-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human; CMV; cytomegalovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            804 CCATGTGACCATGAGGAAATGAGAG 828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CCATGTGACCATTAGGAAATGAGAG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000GB-0004197
2000GB-0018679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001WO-GB00758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 23.4; DB Pred. No. 0.21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 4162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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RESULT 14
AAK77781 standard; D
XX
AAK77781;
XX
AC
AK77781;
A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immune/haematopoietic antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0179065
2000US-0119628
2000US-0184664
2000US-0189874
2000US-0199874
2000US-0199874
2000US-0199874
2000US-0199874
2000US-0199874
2000US-0198123
2000US-0116647
2000US-0116647
2000US-0116880
2000US-0117496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001WO-US01354.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genomic sequence SEQ ID NO:32593
       08-SEP-2000
08-SEP-2000
08-SEP-2000
08-SEP-2000
11-SEP-2000
11-SEP-2000
11-SEP-2000
11-SEP-2000
11-SEP-2000
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11-SEP-2000
11-SEP-2000
11-SEP-2000
12-SEP-2000
21-SEP-2000
22-SEP-2000
23-SEP-2000
25-SEP-2000
25-SEP-2000
27-SEP-2000
29-SEP-2000
29-SEP-2000
29-SEP-2000
29-SEP-2000
29-SEP-2000
29-SEP-2000
29-SEP-2000
29-SEP-2000
29-SEP-2000
20-CCT-2000
21-NOV-2000
     2000US-0231414

2000US-0232081

2000US-0232396

2000US-0232396

2000US-0233396

2000US-02333063

2000US-02333063

2000US-02333063

2000US-02334293

2000US-02344223

2000US-02344274

2000US-02354484

2000US-0235484

2000US-0235484

2000US-0235836

2000US-0236367

2000US-0236367

2000US-0236367

2000US-02363703

2000US-0246476

2000US-0246526

2000US-0249211

2000US-0249211

2000US-0249211

2000US-0249211

2000US-0249211

2000US-0249211

2000US-0249211

2000US-0249211

2000US-0249211

2000US-0249214

2000US-0249214

2000US-0249214

2000US-0249214

2000US-0249214

2000US-0249244

2000US-0249244

2000US-0249244

2000US-0249244

2000US-0249244

2000US-0249244
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AAH93977,
ID AAH9
XX
AC AAH5
XX
DT 05-C
XX
DT 05-C
XX
W noo1
KW genk
KW genk
KW genk
KW genk
KW grov
KW noo1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic CC proteins and polynucleotides may be used in yene therapy and vaccine production. (I) CC treatment of diseases associated with inappropriate (I) expression. For CC expression by rectifying mutations or deletions in a patient's genome CC expression by rectifying mutations or deletions in a patient's genome CC expression by rectifying mutations or deletions in a patient's genome CC expression by rectifying mutations or deletions in a patient's genome CC expression by rectifying mutations or deletions in a patient's genome CC expression by rectifying mutations or deletions in a patient's genome CC expression by rectifying mutations or deletions in a patient's genome CC expression by rectifying mutations or fellower in the patient's genome CC expression by rectifying the patient of the product the secreted (I), by inserting CC concers and caids into a host cell and culturing the cell to express the CC diagnose and treat immune/haematopoletic-related diseases, especially to AAK87694 represent human immune/haematopoletic antigen genomic CC sequences from the present invention. AAK54920 and AAM82169 and AAM82169
                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                26482 CCATGTGACCATGAGGAAATGAGAG 26458
                 Human; foetal protein; cytostatic; immunosuppressive; immunostimulant; nootropic; neuroprotective; thrombolytic; osteopathic; antiinflammator; gene therapy; antisense therapy; cancer; immune disorder; growth disorder; osteoporosis; thrombolytic disorder;
                                                                                                                  Human foetal cDNA, SEQ ID NO: 506.
                                                                                                                                                                                                                          AAH93977 standard; cDNA; 367 BP.
nervous system disorder; inflammation; expressed sequence tag; EST; ss
                                                                                                                                                       05-OCT-2001 (first entry)
                                                                                                                                                                                                 AAH93977;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 27884 BP; 9296 A; 5084 C; 5260 G; 8244 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2000;
01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 32593; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-483426/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-DEC-2000;
08-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                   1 CCATGTGACCATTAGGAAATGAGAG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                               TOCAL
                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0249299.
2000US-0249300.
2000US-0250160.
2000US-0250391.
2000US-0251030.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0254097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0251856.
                                                                                                                                                                                                                                                                                                                                                                                                        93.6%;
96.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                        <u>,,</u>
                                                                                                                                                                                                                                                                                                                                                                                                  Score 23.4; DB 22; Pred. No. 0.27;
                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                     Length 27884;
                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                       antiinflammatory;
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Search completed: March 17, 2003, 10:50:36 Job time: 151.446 secs
                                                                                                                                                                                В
                                                                                                                        Matches
                                                                                                                                                  Query Match
                                                                                                                                                                                         The invention relates to novel foetal polypeptides encoded by polynucleotides comprising one of 477 sequences fully defined in the specification. The foetal polynucleotides and polypeptides are useful in the treatment and diagnosis of diseases such as cancers, immune disorders, growth disorders (e.g. osteoporosis), thrombolytic disorders, nervous system disorders and inflammation. The present sequence was assembled using an expressed sequence tag (EST) found to be expressed in human foetal tissue cDNA libraries as the seed.
                                                                                                                                                                   Sequence 367 BP; 94 A; 65 C; 58 G; 150 T; 0 other;
                                                                                                                                                                                                                                                                                                                              Claim 1; Page 362-363; 715pp; English.
                                                                                                                                                                                                                                                                                                                                                                  Novel fetal proteins useful for the treatment and diagnosis of diseases associated with dysfunction of the protein e.g. cancers, immune disorders, growth disorders, thrombolytic disorders, nervous system
                                                         219 ATGTGACAATTAAGAATAAGAG 197
                                                                                                                                                                                                                                                                                                                                                                disorders and inflammation -
                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; AAM06302.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yeung G,
Liu C, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-JAN-2000; 2000US-0491404
15-SEP-2000; 2000US-0663870
06-NOV-2000; 2000US-0707351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-JAN-2001; 2001WO-US02723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                 3 ATGTGACCATTAGGAAATGAGAG 25
                                                                                                                                 Local
                                                                                                                       20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       2001-465571/50.
                                                                                                                                 Similarity
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Asundi V,
                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Boyle BJ, Arterbu
Zhou P, Werhman T;
                                                                                                                              72.8%;
87.0%;

 Mismatches

                                                                                                                                Score 18.2;
Pred. No. 4
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                                                                                                                                        DB 22; Length 367;
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                                                                                                             Indels
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                                                                                                            0,
                                                                                                         Gaps
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Gapop 10.0 , Gapext 1.0
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ALIGNMENTS

BQ308862.1 GI:20851208 BQ308862.1 GI:20851208 BST. human. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo. 1 (bases 1 to 337) Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J. Shotgun sequencing of the human transcriptome with ORF expressed sequence tags Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000) 2020263 Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922

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SOURCE
ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 348 bp mRNA linear EST 02-MA UI-HF-BNO-alj-d-05-0-UI.rl NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079736 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Eco RI site shown at the beginning of the sequence
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
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Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     www-bio.llnl.gov/bbrp/image/image.html
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National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria; Primates; Catarrhini; 1 (bases 1 to 348)
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Seq primer: puc 18 forward
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: asimpson@ludwig.org.br
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/lab_nost="DH10B (LTI)"
/note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco R:
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                                                                                                                                                                                        /cell_type="germinal center B cells"
/cell_line="MGC85"
                                                                                                                                                                                                                                                                    /clone_lib="NIH_MGC_50"
/tissue_type="lymph"
                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:9606"
/clone="IMAGE:3079736"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
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Pred. No. 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mEST@mail.nih.gov
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/Abb_host="PHIOB (Life Technologies)"
/Abb_host="PHIOB (Life Technologies)"
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/Abb_host="DBIOB (Pharmacia)
/Abb_host="DBIOB (Rife Technologies)
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serially subtracted libraries were gener process: NIH_BMAP_M_S3.3, NIH_BMAP_M_S2, The subtracted library (NIH_BMAP_M_S3.3)
                              subtractions to reduce the representation of cDNAs from which ESTs had already been generated. The following serially subtracted libraries were generated in this process: NIH_BMAP_M_S3.3. WH.BMAP_M_S3.4. NIH_BMAP_M_S3.5.
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/dev_stage="27-32 days"
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/clone="UI-M-BH2.3-any-h-05-0-UI"
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Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D. "
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                                                                                                                                                                                                                                                                                   POLYA-Yes.
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6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
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TAG_TISUE-basal-ganglia
                                                   /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UI-M-BH2.1-apo-a-05-0-UI"
/clone_lib="NIH_BMAP_M_33.1"
/dev_stage="27-32 days"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                         /lab_host-"DH10B (Life Technologies)"
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                                                                                                                                                                                           organism-"Mus musculus"
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COMMENT

JOURNAL MEDLINE TITLE REFERENCE

SOURCE KEYWORDS ACCESSION

ORGANISM

ERSION

DEFINITION AW124493 RESULT 4 BASE COUNT

Matches

FEATURES

COMMENT

JOURNAL

REFERENCE

AUTHORS TITLE

SOURCE KEYWORDS ACCESSION DEFINITION

ORGANISM

VERSION

source

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Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 93.6%; Local Similarity 96.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CCATGTGACCATTAGGAAATGAGAG 25
Email: mEST@mail.nih.gov

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the amygdala tissue cDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Chin, H
Mational Institute of Mental Health
0001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 395)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BE980521 395 bp mRNA linear EST 05-OCT-200 UT-M-BG2-bck-b-03-0-UI.Sl NIH_BMAP_MSC_Sl Mus musculus cDNA clone UI-M-BG2-bck-b-03-0-UI 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           which ESTs had already been generated. The following scrially subtracted libraries were generated in this process: NIH_BMAP_M_S3.1, NIH_BMAP_M_S3.1 NIH_BMAP_MS3.1 NIH_BMAP_MS3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polylinker; Site_1: Not I; Site_2: Eco RI; The NIH_BMAP_M_S3.1 library is a subtracted library of a series, ultimately derived from a mixture of individually tagged normalized libraries from ten regions of the mouse brain (cerebellum, brain stems, olfactory bulbs, bypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hipoccampus) after a series of subtractions to reduce the representation of cDNAs from the context and the con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAG_TISSUE=amygdala
TAG_SEQ=GTGAG"
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Pred. No. 2.
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RESULT 5 BE980521

ocus

ORIGIN BASE COUNT

Matches

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
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                                                                                                                                                          source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BF406698 501 bp mRNA linear EST 28-NOV-UI-R-BJ2-bpo-b-02-0-UI.s1 UI-R-BJ2 Rattus norvegicus cDNA clone UI-R-BJ2-bpo-b-02-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                limited collaborative arrangements
                                                                                                                                                                                                                                                                                                    Email: msoares@blue.weeg.uiowa.edu
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: clones will be available through
Research Genetics (www.resgen.ccm) The following repetitive
elements were found in this cDNA sequence: 25-96, >B1-F#SINE/Alu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Soares, MB
program for Rat Gene Discovery and Mapping
University of Iowa
451 Bokstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97044477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bonaldo,M.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BF406698.1 GI:11394673
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                                                                                                                                                                                                                                         POLYA=No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 501)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  108
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/clone_lib="NIH_BMAP_MSC_S1"
/dev_stage="27-32 days"
/lab_host="DHIDB (Life Technologies)"
/lab_host="DHIDPAC"
/lab_host="DHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAG_SEQ=GTGAG<sup>*</sup>
1 73 c
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/strain="C57BL/6J"
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/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-BJ2-bpo-b-02-0-UI"
                                                                                                                      /organism="Rattus norvegicus"
                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lennon, G. and Soares, M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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Pred. No. 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST 28-NOV-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CCATGTGACCATTAGGAAATGAGAG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AT481068 591 bp mRNA linear EST 09-MAR-1999 vf92d03.x1 Soares_mammary_gland_NDMMG Mus musculus cDNA clone IMAGE.851237 3' similar to TR:008741 008741 HYPOXIA-INDUCIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 591)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Possible reversed clone: similarity on wrong strand High quality sequence stop: 472.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AI481068.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone was previously sequenced on the 5' end only, this new data is from the 3^{\prime} end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGI:503389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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/lab_host="bHi0B (Life Technologies)"
/lab_host=
T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="mammary gland"
/dev_stage="4 weeks"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:10090"
/clone="IMAGE:851237"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                               note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia with a modified polylinker; Site_1: Not I; Site_2: Eco
                                                                                                                                                                                                                                                                                                                                                                                                             /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Soares_mammary_gland_NbMMG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GI:4374294
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96.0%;
                                                                                                                                                                                                                                                                                       th a modified polylinker; Site_1: Not I; Site_2: Ec 1st strand cDNA was primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 23.4; DI
Pred. No. 3.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
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                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           390 CCATGTGACCATGAGGAAATGAGAG 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CCATGTGACCATTAGGAAATGAGAG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plate: 63 row: B column: 11 High quality sequence stop: 684.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 684)

Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: yongsung@mail.kribb.re.kr
Plate: 63 row: B column: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Kim YS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21C Frontier Korean EST Project 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       K-EST0109485 S11SNU1 Homo sapiens cDNA clone S11SNU1-63-B11 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BM834484.1 GI:19190893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 numan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
        Conservative
                                                                                                                /note--organi Stomach; Vector: pME18-FL3; Site_1: XhoI; Site_2: XhoI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including Sfil site by treatment of 74 RNA ligase and the first strand cDNA was synthesized with Superscript II using Sfil oligo-dT primer. After first strand synthesis, RNA was degraded by NaOH treatment and cDNA was amplified by PCR reaction. The PCR products were digested with Sill and cloned into DraIII- digested pME18S-FL3 vector. The competent cells E. coll ToplOF by electroporation method. The CDNA libraries constructed by this method are full-length enriched cDNA library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cell_type="Lymphoblast-like"
/cell_line="SNU-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="S11SNU1-63-B11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="Top10F'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="Stomach"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="S11SNU1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bonaldo."
                        93.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93.68;
                                                                                                              135 c
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                        Score 23.4; DB 14; Length 684; Pred. No. 3.6;
                                                                                                         136 g
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Pred. No. 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
Normalization, Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
                                                                                                                                                                                                                                                         cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosaiwa, H., Yamanaka, I., Alzawa, K., Fikuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. . 10 (11), 1757-1771 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
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Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda
,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki
,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTS (Arakawa,T., et al. 2001)
On Jun 30, 2000 this sequence version replaced g1:8864855.
                                                                                                                                                                                                                                                                                                                                                                                                         Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hayashizaki, Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Y. and Hayashizaki,Y.
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Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Laboratory for Genome Exploration Research Group, RIKEN Genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Computer-based methods for the mouse full-length cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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/clone_lib="RIKEN full-length enriched, 0 day neonate thymus" \label{eq:clone_lib}
                                                                    /db_xref="taxon:10090"
/clone="A430018A13"
                                                                                                                                  organism="Mus musculus"
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414 CCATGTGACCATGAGGAAATGAGAG 438
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                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) CDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                               Plate: LLCM534 row: o column: 11
High quality sequence stop: 697.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/dev_stage="0 day neonate"
/lab_host="DH10B"
/tissue_type="choriocarcinoma"
/tissue_type="choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
/note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
/note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
/note="Organ: placenta; Vector: pOTB7; Site susing the Directionally cloned into EcoRI/XhoI sites using the Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University Ling Hong in the laboratory of Gerald M. Rubin (University California, Berkeley) using ZAP-cDNA synthesis kit
                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone_lib="NIH_MGC_21"
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
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602986733F1 NCI_CGAP_Lu33 Mus musculus cDNA clone IMAGE:5142800 5',
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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/db_xref="taxon:10090"
/clone="IMAGE:4223096"
/clone=NCI_CGAP_Kid14"
/lab_host="DH10B (T1 phage=resistant)"
/lab_host="UH10B (T1 phage=resistant)"
/lab_lost="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="FVB/N"
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Pred. No. 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
            Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
                                                                                                                 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 769)
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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High quality sequence stop: 726.
Location/Qualifiers
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DNA Sequencing by:Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11352 row: a column: 09
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Tissue Procurement: Gilbert Smith, ph.D.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/db_xref="taxon:10090"
/clone="IMAGE:5142800"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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1 (bases 1 to 791)
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Clone distribution: MGC clone distribution information can be
found through the r.m.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAN10770 row: h column: 12
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/organism="Homo saplens"
/db_xref="taxon:9606"
/clone=_in_akgE:4367229"
/clone_ib="NHH_MCC_86"
/tissue_type="osteosarcoma, cell line"
/tissue_type="osteosarcoma, cell line"
/lab_host="DH10B (phage=resitant)"
/note="organ: bone; Vector: pcMv-SpORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally; oligo-dr primed.
Average insert size 1.533 kb. Library enriched for
full-length clones and constructed by Life Technologies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-"Organ: testis; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhOI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTVN-3', size-selected for average insert size 2.2 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMF/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                              Location/Qualifiers
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/lab_host="DH10B"
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Best Local Similarity
Search completed: March 17, 2003, 13:09:12 Job time : 888.737 secs
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Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: genomics@hri.co.jp
HRI human cDNA project; 5'. & 3'.end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
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Unpublished (2000)
Contact: Takao Isogai
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1 145 c 173 g 223 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cell_type="teratocarcinoma"
/cell_line="NT2"
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/clone_lib="NT2RP3"
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/db_xref="taxon:9606"
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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## ALIGNMENTS

AUTHORS BOSS TITLE CONV	Phil REFERENCE 1 (	Euka Ampl	ORGANISM Phil	SOURCE Phil	KEYWORDS .	VERSION AF24	ACCESSION AF24	DEFINITION Phil	LOCUS AF24	AF249160	RESULT 1
Bossuyt, F. and Milinkovitch, M.C. Convergent Adaptive Radiations in Madagascan and Asian Ranid Frogs	Philautus. 1 (bases 1 to 175)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rhacophoridae;	Philautus charius	Philautus charius.		AF249160.1 GI:12247249	AF249160	•	AF249160 175 bp DNA linear VRT 17-JAN-2001		

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AUTHORS
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Submitted (27-MAR-2000) Unit of Evolutionary Genetics, Institute
                                                                                                                                                                                                                                                                           Submitted (25-JAN-1999) S.N. Archer, International Marine Centre, Localita sa Mardini, 0972 Torregrande, Oristano, ITALY
                                                                                                                                                                                                                                                                                                                             Archer, S.N.
                                                                                                                                                                                                                                                                                                                                                             Unpublished
                                                                                                                                                                                                                                                                                                                                                                            Comparative analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Clupeomorpha; Clupeidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sardina pilchardus
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Bossuyt, F. and Milinkovitch, M.C.
                                                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 1056)
Archer,S.N. and Hirano,J.
                                                                                                                                                                                                                                                                                                                                                                                                                               Sardina
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FVFGRMGCNIEGFFATLGGEIALWSLVVLSMERWIVVCKPISNFRFGENHAVMGVAFS
WFMAAACAVPPLYGWSRYIPEGMQCSCGIDYYTRAGOTNNESFYNYTHTVHFTCPLTI
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                                                                                                                                               function="phototransduction"
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Kawamura, S., Blow, N.S. and Yokoyama, S. Genetic analyses of visual pigments of the pigeon (Columba livia) Genetics 153 (4), 1839-1850 (1999)
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AF149230
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/note="degenerate primer"
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                                                                                                                                                                                                                                      AL Submitted (11-JUL-2001) Makiko Suwa, Computational Biology Research Center (CBRC), National Institute of Advanced Industrial Science and Technology (AIST); 2-41-6 Aomi Koto-ku, Tokyo 135-0064, Japan (E-mail:m-suwa@aist.go.jp, URL:http://www.cbrc.jp/, Tel:81-3-3599-8080, Fax:81-3-3599-8081)
This sequence is a seven transmembrane helix receptor candidate predicted from the whole human genome sequences using our automated system that contains programs of gene finding(GeneDecoder), sequence search, motif-domain assignment and transmembrane helix prediction.

And the sequence is submitted by the collaborative project between (Computational Biology Research Center (CBRC), National Institute of Advanced Industrial Science and Technology (AIST) and [Genome Technology (RAST), University of Tokyo].
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
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Dryja,T.P. and Berson,E.L.
Diagnosis of hereditary retinal degenerative diseases
Patent: US 5498521-A 1 12-MAR-1996;
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/evidence=not_experimental
/product="seven transmembrane helix receptor"
/protein_id="BACOS894.1"
/db_xref="GI:21928611"
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                                                                                                                              /db_xref="taxon:9606"
/chromosome="3"
                                                                                      /codon_start=1
                                                                                                                 )oin(201.
                                                                                                                                                                          /isolate-"CBRC7TM_
                                                                                                                                                                                          ∕organism="Homo sapiens"
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95.7%;
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Submitted (22-FEB-1996) Jeremy Nathans, Molecular Biology and Genetics, Johns Hopkins Medical School, 725 N. Wolfe Street, Baltimore, MD 21205, USA
On Sep 3, 1996 this sequence version replaced gi:189393.
                                                                             Direct Submission
                                                                                             Nathans,J
                                                                                                                             658963
                                                                                                                                              84272729
                                                                                                                                                                                                       Nathans, J. and Hogness, D.S.
                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                        U49742.1
                                                                                                                                                                                                                                                                                                                                    Human rhodopsin gene, complete cds. U49742 K02281
                                                                                                                                                                         rhodopsin
                                                                                                                                                                               Isolation and nucleotide sequence of the gene encoding human
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Dryja, T.P. and Berson, E.L.
Diagnosis of hereditary retinal degenerative diseases
Patent: US 5498521-A 2 12-MAR-1996;
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Sequence 2 from patent US 5498521.
I18747
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2022 c 1797 g
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В

Bryant, N.P., Bonnin, D.

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/protein_id="aaC31763.1"
/protein_id="aaC31763.1"
/db_xref="G1:1236137"
/td=ns1ation="mmGTEGPNEYVPESNATGVVRSPFEYPQYYLAEPWQFSMLAAYM
/translation="mmGTEGPNEYVPESNATGVVRCKPMSNERFESHATMTSLHGY
FLLTVLGFPINFITLYVTVQHKKLRTPLNYILLALAVADLFMVLGGFTSTLYTSLHGYAFT
FVFGPTGCNLEGFFATLGGETALWSLVYLALBRYVVVCKPMSNERFGESHAIMGVAFT
FVFGPTGCNLEGFFATLGGETALWSLVYLAURGTTPAUM
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join(295. .655,2439. .2607,3813. .3978,4095. .4334,5168. .5278)
/note="the 5 exons of the human rhodopsin gene are similar to the 5 exons of the Bos taurus opsin gene"
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IFFCYGQLVFTVKEAAAQQQESATTQKAEKEVTRMVILMVIAFLLCWVPYASVAFYIF
THQGSNFGPIFMTIPAFFAKSAAIYNPVIYIMMNKQFRNCMLTTICCGKNPLGDDEAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="rhodopsin mRNA (alt); the 5' untranslated region is
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5642. .56
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                                                                                                                                                                                                                                                                                                                                                          /note-"potential polyA signal"
/6698. 6903
/note-"potential polyA signal"
<sub>1</sub> 2022 c 1796 g 1611 t
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/note="intron D; the four introns present in both the /note="intron D; the four introns present in both the human and the bovine genes occur at precisely analogous bositions and are of comparable lengths"
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/note="intron
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95.7%;
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                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                    DB 9; Length 6953;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Douthwaite, K. J., Draper, H., Dugan Woche, N., Durbin, N., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Schotto, M., Garcha, A., Garner, P., Garza, N., Gill, R., Gabisi, A., Gao, J., Garcia, A., Garner, P., Hale, S., Hamilton, K., Gorrell, J. H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Gorrell, J. H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Harris, C., Harris, C., Harris, K., Holloway, C., Hollins, B., Harris, C., Harris, K., Huber, J., Hulyk, S., Hume, J., Jackson, L. E., Homsi, F., Hodgson, A., Hogues, M., Holloway, C., Joudah, S., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlyson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Lizado, R., Juna, R., Ma, J., Lozado, R., J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Lozado, R., J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Lozado, R., J., Lu, X., Lucier, A., Lucier, R., Martindale, A., Martinez, E., Mahshwari, M., Mapua, P., Martin, R., Magdor, M., Moris, S., Massey, E., Mahhari, M., Magdor, M., Moris, S., Mayuen, N., Nickerson, J., Newtson, N., Nguyen, A., Nguyen, N., Mosey, M., Nowaha, P., Meador, N., Nguyen, A., Nguyen, N., Nickerson, J., Newtson, N., Nguyen, A., Nguyen, N., Nguyen, A., N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bong
Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Brye
Buhay, C., Burch, P., Burkett, C., Burrell, L., Byrd, N.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 163297)
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HOMO sapiens chromosome 3 clone RP11-26311, WORKING DRAFT SEQUENCE,
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                                                                                                                                                                                                                 Submitted (24-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                               Submitted (09-FEB-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 163297)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Worley, K.C.
                                                                                                                                                                                     Jul 19, 2002 this sequence version replaced gi:20127313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 163297)
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                                                                                                                 Center: Baylor College of Medicine
Contact: hgsc-help@bcm.tmc.edu
                           Web site: http://www.hgsc.bcm.tmc.edu/
prafting Center Code: BCM
                                                                                                Center code: BCM
                                                                                                                                                                    Genome Center
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Department

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REFERENCE
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        JOURNAL
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                                                                                                                  l (bases 1 to 164396)

Evans G.A. Bradbury, P., Brignac, S., Bumeister, R., Davie, J.,
Davies, C.J., Davis, C., English, C., Fondon, T., Franklin, T.L.,
Garner, H.R., Gordon, M., Gotway, G., Grant, O., Hahner, L., Harris, J.,
Hinson, S., Megarity, C., Narayanaswamy, U., Newton, J., O'Brien, K.,
Schilling, Probst, S., Rayner, S., Schageman, J.,
Schilling, S., Rayner, S., Schageman, J.,
Schilling, S., Rayner, S., Schageman, J.,
Unpublished
                                                                      Schilling, P., Schultz, R., Syed, M., Valenzuela, D., Ward, T., Wilson, R. and Burbee, D.
                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HOMO Sapiens chromosome 3 clone pDJ70ill, *** SEQUENCING IN ACONO220
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* NOTE: This is a 'working draft' sequence. It currently

* consists of 4 contigs. The true order of the pieces

* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   * NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             be preserved.
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Center project name: HAEW
Center clone name: RP11-2631
Summary Statistics
Sequencing vector: Plasmid;
Sequencing vector: M13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HTGS_PHASE1
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Chemistry: Dye-terminator Big Dye: 87% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 16558 bases at least 040
Consensus quality: 162613 bases at least 030
Consensus quality: 163127 bases 030
Consensus quali
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2734
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57018
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/chromosome="3"
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2733: gap of unknown length
22721: contig of 19988 bp in length
22821: gap of unknown length
57017: contig of 34196 bp in length
57117: gap of unknown length
16297: contig of 106180 bp in length.
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95.7%; Pred. No. 11
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RS Muzny, D.M. Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Bieve, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Escotto, M., Gariel, J.H., Guevara, W., Guararde, P., Hale, S., Hamilton, K., Harris, K., Hart, M., Haves, A., He, X., Hollins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 168551)
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168551 bp DNA linear PRI 07-MAR-2002
HOMO Sapiens 3q BAC RP11-529F4 (Roswell Park Cancer Institute Human
BAC Library) complete sequence.
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* NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
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Evans,G.A., Bradbury,P., Brignac,S., Bumeister,R., Davie,J.,
Davies,C.J., Davis,C., English,C., Fondon,T., Franklin,T.L.,
Garner,H.R., Gordon,M., Gotway,G., Grant,O., Hahner,L., Harris,J.,
Hinson,S., Megarity,C., Narayanaswamy,U., Newton,J., O'Brien,K.,
Oliver,T., Patel,P., Probst,S., Rayner,S., Schageman,J.,
Schilling,P., Schultz,R., Syed,M., Valenzuela,D., Ward,T.,
Wilson,R. and Burbee,D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="pDJ70111"
38527 a 43485 c 42989;
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7835 7934: gap of 100 bp
7935 164396: contig of 156462 bp in lengt
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95.7%;
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Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Lewis, L., Kily, J., Liu, W., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Lowis, L., Li, J., Liu, X., Lucier, A., Lucier, R., Lucier, R., Lucier, R., Lucier, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Maner, C., Miner, Z., Mitchell, T., Mohabbat, K., Meir, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Melo, G., Metzker, M., Miner, C., Miner, Z., Mitchell, T., Mohabbat, K., Melo, G., Metzker, M., Morris, S., Moser, M., Neal, D., Nickerson, E., Novsenko, S., Oguh, M., Okwuonu, G., Oragunye, N., Nickerson, E., Novsenko, S., Oguh, M., Okwuonu, G., Oragunye, N., Nickerson, E., Novsenko, S., Oguh, M., Okwuonu, G., Oragunye, N., Nickerson, E., Novsenko, S., Oguh, M., Okwuonu, G., Oragunye, N., Pikens, R., Primus, E., Pu, L., Quiles, M., Ren, Y., Rives, M., Pitches, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Stone, H., Sutton, A., Svatek, A., Sonaike, T., Sparka, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, P., Tannerisa, A., Tamerisa, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Walliams, G., Wu, Y., Walliamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wulliamson, A., Svarilla, S., Naylor, S.L., Weinstock, G. and Gibbe, R.
Direct Submission
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JOURNAL REFERENCE REFERENCE TITLE JOURNAL TITLE AUTHORS Submitted (23-SEP-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA Unpublished 2 (bases 1 Direct Submission Worley, K.C. (bases 1 to 168551) (bases 1 to 168551)

JOURNAL AUTHORE Submitted (31-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA Worley, K.C. Direct Submission

REFERENCE

Submitted (07-MAR-2002) Human Genome Sequencing Center, Depar of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA on Nov 30, 2001 this sequence version replaced gi:16572867. gc-help@bcm.tmc.edu INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email Submission Department

COMMENT

JOURNAL

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searc of a local database that includes entries from dbSTS, GDB, and 7:541-550) searches

local mapping efforts.

unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES:This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found quality are listed below. Description of the metrics can be found to the control of the metrics can be found that ITL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.

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                                                                                                                                                                                    Submitted (14-APR-1997) Molecular Genetics, Ophthalmology, Bath
Street, London ECIV 9EL, UK
                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                           Hunt, D.M., Fitzgibbon, J., Slobodyanyuk, S.J., Bowmaker, J.K. and
                                                                                                                                                                                                                                                                                                              deduced from nuclear DNA evidence
Mol. Phylogenet. Evol. 8 (3), 415-422 (1997)
                                                                                                                                                                                                                                                                                                                                      Molecular evolution of the cottoid fish endemic to Lake Baikal
                                                                                                                                                                                                                                                                                                                                                                       Hunt, D.M., Fitzgibbon, J., Slobodyanyuk, S.J., Bowmaker, J.K. and
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    AF249133.1 GI:12247195
                     Mantella madagascariensis rhodopsin gene, exon 4 and partial
                                              AF249133
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Bossuyt,F. and Milinkovitch,M.C.
Convergent Adaptive Radiations in Madagascan and Asian Ranid Frogs
Reveal Co-variation between Larval and Adult Traits
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/protein_id="AAG49773.1"
/db_xref="GI:12247190"
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Bossuyt, F. and Milinkovitch, M.C.
Convergent Adaptive Radiations in Madagascan and Asian Ranid Frogs
Reveal Co-variation between Larval and Adult Traits
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Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rhacophoridae;
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Bossuyt, F. and Milinkovitch, M.C
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Bossuyt,F. and Milinkovitch,M.C.
Convergent Adaptive Radiations in Madagascan and Asian Ranid Frogs
Reveal Co-variation between Larval and Adult Traits
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rhacophoridae;
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Bossuyt, F. and Milinkovitch, M.C.
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/protein_id="AAG49776.1"
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/product="rhodopsin" <1. .>175
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Search completed: March 17, 2003, 11:25:45 Job time: 313.903 secs
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                                                        Local
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                                                                                                                                                                                                                                                                                                                                                                                                     Bossuyt,F. and Milinkovitch,M.C. Direct Submission Submitted (27-MAR-2000) Unit of Evolutionary Genetics, Institute of Molecular Biology and Medicine, rue Jeener and Brachet 12, Gosselles B-6041, Belgium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AF249136.1 GI:12247201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Boophis xerophilus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rhacophoridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Boophis xerophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                             /product="rhodopsin" <1. .>175
                                                                                                                                                                                       /number=4
a 55 c
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                                                                                                                                                                                                                                                                                                                                                                 /organism="Boophis xerophilus"
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91.3%;
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                                                                                                                                Score 19.8;
Pred. No. 37
                                                                                                                    0; Mismatches
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
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                    Score
                                                                                                                                                                          d. No. 1s the number of results predicted by chance to have a
re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
                 Match
                                                   Query
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Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                            1: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
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24
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                                                                                                                                                                by analysis of the total score distribution.
          Length
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Description
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956 2013 2060 2060 5801

ABV34093 ABV42957 AAA44043 ABA12912 ABA18522 ABA18522 ABV22500 ABV28314

AAH84028 AAA57090 ABN73103

ALIGNMENTS

Human breast Human colon cancer Bovine embryonic g Eulemar fulvus olf Human prostate exp

AAZ93310 AAA57072 ABV06135 AAL13938

Human

Sequence encoding Human colon cancer Human prostate exp 385 433

1845 4785 4785 4786 4786 4786 4786 4785 4785 4785 34185 240825 240823

ABN6662 AATT3631 AAQ14942 AAQ14942 AAQ48794 AAQ48794 AAQ48796 AAQ48796 AAQ48797 AAQ48797 AAQ48797 AAQ48797 AAQ48797

ABK80749 AAK59608 ABL02990 ABK80729

Streptococcus poly Human p65 oncofoet Human immune/haema Bacillus clausii Bacillus clausii Drosophila melanog Drosophila melanog Rat sequence Human

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prostate exp equence diffe prostate

Cyclodextrin gluca
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misc_binding	<pre>primer_bind CDS</pre>	Key 5'UTR 5'UTR	Human; rhodopsi probe; primer; eye; rod; retin Homo sapiens.	06-JUL-1996 (f	RESULT 1 AAT17115 ID AAT17115 standard; DNA; 3016 XX XX AC AAT17115; XX
/*tag= d /product= Rhodopsin complement (354372) /*tag= e /note= "Binds probes AAT17117 (mutant) and AAT17118 (normal)"	complement (231250)  /*tag= c /note= "Binds primer 348 (AAT17121)" 2955278	Location/Qualifiers 200.294 /*tag= a 202.294 /*tag= b	Human; rhodopsin; transversion; mutation; retinitis pigmentosa; probe; primer; hybridisation; polymerase chain reaction; PCR; eye; rod; retina; diagnostic; prenatal diagnosis; photoreceptor; ds. Homo sapiens.	(first entry)	ard; DNA; 3016 BP.

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9 6 7 6 U A U A L

21.4 21.4 18.8 18.2 11.2 17.6 17.4 17.4

89.2 89.2 78.3 75.8 75.8 72.5 72.5

3016 6953 8641 3129 3190 3190 1563 2209 2601 36135

17 20 14 23 23 22 20 20 20

AAT17116 AAX84344 AAQ43543 ABL26876 AAZ53713 AAS41923

Rhodopsin gene. H Rhodopsin gene. H Stealth virus nucl Rhodopsin gene. H Drosophila melanog Neisseria gonorrhe

Genomic sequence # Fervidobacterium p 1mmune/haema

**AAT17115** 

misc_binding

US5498521-A

24-JAN-1990; 12-MAR-1996 primer_bind

mutation

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pigmentosa. Probes AAT17117 and AAT17119 bind transversion mutation sequence, and probes AAT17118 and AAT17118 and AAT17120 bind transversion mutation sequence, and probes AAT17118 and AAT17120 and 502 (AAT17123) may be used along with primer 348 (AAT17121) to amplify mutant and normal sequences, respectively, by PCR. Mutations in the retinal degeneration slow protein and retinal rod cGMP-phosphodiesterase genes are also implicated in retinitis pigmentosa. Detection of any of these mutations in a foetus or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence encodes human rhodopsin, and is shown without introns. The full sequence, with introns, is shown in AAT17116. Substitution of histidine for the normal nonpolar amino acid proline at position 23, by substitution of C with A in codon-23, results in a dysfunctional or absent molecule, affecting rod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Diagnosis of hereditary retinal degenerative diseases e.g. retinitis pigmentosa, - caused by a human photoreceptor protein mutation, by detection of the mutation by PCR amplification or hybridisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-JAN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAR93116.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1996-159684/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HARD ) HARVARD COLLEGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3016 BP; 689 A; 863 C; 753 G; 711 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Column 19-24; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              patient may be used in diagnosis.
    Rhodopsin gene
                                                   06-JUL-1996 (first entry)
                                                                                                                                        AAT17116 standard; DNA; 6953 BP
                                                                                                                                                                                                                                                                                                  1 GCTTTCTTTGCCAAGAGCGCCGC 23
                                                                                                                                                                                                                                                       GCGTTCTTTGCCAAGAGCGCCGC 1190
                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                            Conservative
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90US-0469215.
91US-0805123.
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/*tag= f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note- "Binds primers 485 (AAT17122) (normal) and 502
                                                                                                                                                                                                                                                                                                                                                                      89.2%;
95.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (mutant)"
                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                    Score 21.4; DB 17; Length 3016; Pred. No. 1.7;
                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                     0;
Human; rhodopsin; transversion; mutation; retinitis pigmentosa; intron; probe; primer; hybridisation; polymerase chain reaction; eye; rod; retina; diagnostic; prenatal diagnosis; photoreceptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5'UTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                 11-MAR-1993;
24-JAN-1990;
11-DEC-1991;
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  WPI; 1996-159684/16
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                                            Berson EL, Dryja TP;
                                                                                    (HARD ) HARVARD COLLEGE
                                                                                                                                    93US-0033081.
90US-0469215.
91US-0805123.
                                                                                                                                                                                                                           90US-0469215
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/note= "Alternative 5'-UTR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
200..294
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/number= 2
2608..3812
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2439..2607
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Binds probes AAT17119 (mutant) and AAT17120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Binds probes AAT17117 (mutant) and AAT17118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /number= 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      295..655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          202..294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                666..2438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Binds primers 485 (AAT17122) (normal) and 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Binds primer 348 (AAT17121)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note=
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"Substitution with A in mutant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (mutant)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence"
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AAT17116 ID AAT1

XEXTXXX

AAT17116;

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1168

Query Match Best Local Matches

Berson EL,

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This sequence represents a Stealth virus nucleic acid clone. The invention relates to a method of detecting and characterising a stealth virus by reacting a sample suspected of containing a stealth virus with probe from a known stealth virus and sequencing the resultant isolated nucleotide. The method comprises the steps of: (a) isolating DNA or RNA
                                                                                                   Claim 19; Page 76-79; 95pp; English.
                                                                                                                                    Novel strains of stealth virus
                                                                                                                                                                      WPI; 1999-405521/34.
                                                                                                                                                                                                                                  (MART/) MARTIN W J.
                                                                                                                                                                                                                                                                30-DEC-1997;
                                                                                                                                                                                                                                                                                             30-DEC-1998;
                                                                                                                                                                                                                                                                                                                            08-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                     Stealth virus.
                                                                                                                                                                                                                                                                                                                                                                                                       Stealth virus; detection; diagnosis; infection; ss
                                                                                                                                                                                                                                                                                                                                                        W09934019-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Stealth virus nucleic acid clone, SEQ ID NO: 36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-SEP-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAX84344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAX84344 standard; DNA; 8641 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4272 GCGTTCTTTGCCAAGAGCGCCCC 4294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transversion mutation sequence, and probes AAT17118 and AAT17120 bind to the corresponding normal sequence. Primers 485 (AAT17122) and 502 (AAT17123) may be used along with primer 348 (AAT17121) to amplify retinal degeneration slow protein and retinal red cGMP-phosphodiesterase genes are also implicated in retinitis phosphodiesterase genes are also implicated in a foetus or national manual forms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6953 BP; 1523 A; 2022 C; 1797 G; 1611 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              patient may be used in diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         codon 23, results in a dysfunctional or absent molecule, affecting rod function, and is linked with autosomal dominant retinitis pigmentosa. Probes AAT17117 and AAT17119 bind to the C-to-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence encodes human rhodopsin, and is shown in full with introns. The corresponding sequence without introns is shown in AATI7116. Substitution of histidine for the normal nonpolar amino acid proline at position 23, by substitution of C with A in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Diagnosis of hereditary retinal degenerative diseases e.g. retinitis plymentosa, caused by a human photoreceptor protein mutation, by detection of the mutation by PCR amplification or hybridisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Column 23-30; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAR93116.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GCTTTCTTTGCCAAGAGCGCCGC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                           97US-0001184.
                                                                                                                                                                                                                                                                                          98WO-US27744.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89.2%;
95.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 21.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 6953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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The sequence given represents the human rhodopsin cDNA. Mutant versions of this sequence encode proteins which cause retinal degeneration. These sequences may be identified using primers/probes described in the invention (see also AAQ43545-48) and may be used to diagnose hereditary retinal degeneration. This sequence is the closest approximation to the gene sequence as the sequence given in the specification is not printed clearly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                              Disclosure; Fig 1; 56pp; English.
                                                                                                                                   Probe or primer contg. sequence of human retinal degeneration slow protein mutant - used to diagnose hereditary retinal degenerative diseases
                                                                                                                                                                                                                                    Berson EL, Dryja TP;
                                                                                                                                                                                                                                                              (HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                         11-DEC-1991;
                                                                                                                                                                                                                                                                                                                  08-DEC-1992;
                                                                                                                                                                                                                                                                                                                                           24-JUN-1993.
                                                                                                                                                                                                                                                                                                                                                                      W09312134-A.
                                                                                                                                                                                                                                                                                                                                                                                                                               prim_transcript 200.1341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8149 CTTTCTTTCGCAAGAGCGCCGC 8170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from a sample suspected of containing a stealth virus, e.g. a culture of cells showing a viral cytopathic effect; (b) testing the reactivity of the isolated DNA or RNA with a molecular probe that contains at least 18 identified from a stealth virus; and, optionally (c) sequencing the used to detect stealth virus in a biological product, food or in the inhibitory or stimulatory effects on stealth virus replication and to the nucleic acid sequences of a cell or bacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hereditary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rhodopsin gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-NOV-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAQ43543 standard; cDNA; 3129 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   нuman;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8641 BP; 2101 A; 2031 C; 2018 G; 2476 T; 15 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 CTTTCTTTGCCAAGAGCGCCGC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                            1993-214088/26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rhodopsin; mutant; retinal degeneration; primer; probe;
                                                                                                                                                                                                  AAR38483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                      91US-0805123
                                                                                                                                                                                                                                                                                                               92WO-US10536
                                                                                                                                                                                                                                                                                                                                                                                                       /*tag=
295..12
                                                                                                                                                                                                                                                                                                                                                                                                         .1341
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Pred. No. 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 8641;
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Matches
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                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1168 GCGTTCTTTGCCAAGTCCGCCGC 1190
                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABL26876 standard; DNA; 3190 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster genomic polynucleotide SEQ ID NO 32101.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABL26876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pharmaceutical; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-MAR-2002 (first entry)
                                                                                                                                                                                                         The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 32101; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                       Sequence 3190 BP; 831 A; 719 C; 649 G; 991 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                       2504 CTTTCTTGGCCAAGAGTGCAGCA 2526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GCTTTCTTTGCCAAGAGCGCCGC 23
                                                                                               Local
                                                   2 CTTTCTTTGCCAAGAGCGCCGCA 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adams M,
                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75.8%;
87.0%;
                                                                                                  75.8%;
87.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 18.2; DB 14; Length 3129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No.

 Mismatches

                                                                                                   Score 18.2;
pred. No. 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61;
                                                                                                                    DB 23; Length 3190;
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                                                                                           Indels
                                                                                                                                                                                                                                                                                                            The invention is
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                                                                                             Gaps
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                                                                                                                                                                                      AAS41923
ID AAS4
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                             RESULT 7
                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine; antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neisseria gonorrheae ORF 506 partial DNA sequence SEQ ID NO:1375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-MAR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antibacterial; gene therapy; ds.
                                                                                                                                                                                                             represent novel Neisseria meningitis and N. gonorrheae polypucleotides and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ5473 represent and polypeptides. AAZ54573 to AAZ54576 and AAZ54616 to AAZ5473 represent polypeptides, the polypucleotides, antibodies and compositions. The polypeptides are compositions of the invention can be used as vaccines, as diagnostic reagents, and as the invention compositions. The polypeptides can be used in the immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to manufacture of medicaments for treating or preventing infection due to presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-JUL-1998;
02-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9957280-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neisseria gonorrheae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tettelin H, Venter JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                       AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941
                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 7; Page 748; 1453pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel Neisserial polypeptides predicted to be useful antigens vaccines and diagnostics \bar{\phantom{a}}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAY74951.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      petersen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fraser C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GENO-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CHIR ) CHIRON CORP
                                                                                                                                                                                      Sequence 1563 BP; 287 A; 372 C; 487 G; 417 T; 0 other;
   AAS41923 standard; DNA; 2209 BP
                                                                         63 GCTTTGTTTGACAACACCGCCGCA 40
                                                                                                   1 GCTTTCTTTGCCAAGAGCGCCGCA 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000-062150/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INST GENOMIC RES.
                                                                                                                                             h
73.3%; Score 17.6; DB 21; Length 1563;
Similarity 83.3%; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Galeotti C, Grandi G,
Pizza M, Rappuoli R,
                                                                                                                                      Conservative
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98US-0103794.
98US-0103796.
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98US-0099062.
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 Mismatches

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, Ratti G,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , Mora M;
Scarselli
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AAZ53713/c RESULT 6 IJ

AAZ53713 standard; DNA; 1563 BP

AAS41923;

Gaps

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tic sequence #239 encoding novel human enzyme polypeptide.    Oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase; munue disorder; neuricajicatii admunodeficiency disorder; munue disorder, neuricajicatii admunodeficiency disorder; munue disorder, neuricajicatii admunodeficiency disorder; munue disorder, neuricajicati admunodeficiency disorder; arthritic; neuricajicati disorder gene encodericatic; sepicase disorder; neuricajicatos disorder; gene encodericatic; sepicase disorder; neuricajicaticaticaticaticaticaticaticaticaticat
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14-SEP-2000; 14-SEP-2000; 14-SEP-2000; 14-SEP-2000; 14-SEP-2000; 14-SEP-2000; 21-SEP-2000; 21-SEP-2000; 25-SEP-2000; 26-SEP-2000; 27-SEP-2000; 29-SEP-2000; 20-OCT-2000; 21-NOV-2000;
D. 2000US-0232398. 2000US-0232399. 2000US-0232401. 2000US-0233063. 2000US-0233063. 2000US-0233063. 2000US-0234293. 2000US-0234293. 2000US-0235836. 2000US-0235836. 2000US-0236369. 2000US-0236369. 2000US-0236369. 2000US-0236369. 2000US-0236369. 2000US-0236369. 2000US-0236369. 2000US-0236369. 2000US-0246379. 2000US-024677. 2000US-0246611. 2000US-0246236. 2000US-02462

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RESULT 8
AAX30035/c
ID AAX3900
AC AAX900
XX 17-SEP
XX 17-SEP
XX Fervid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to the isolation of novel human enzyme CC polypeptides (AAUZ2915-AAUZ3814), and the cDNA and genomic sequences CC encoding them. The enzyme polypeptides of the invention may comprise the CC encoding them. The enzyme polypeptides of the invention may comprise the CC disorders or ligases. The sequences of the invention are useful in the CC disorders including hyperproliferative disorders (e.g. cancer), CC disorders including hyperproliferative disorders (e.g. cancer), CC (e.g. arthritis), neurological disorders (e.g. disorders (e.g. cancer), CC (e.g. arthritis), neurological disorders (e.g. inflammatory disorders (e.g. asthma), cardiovascular disorders (e.g. atherosclerosis), CC (e.g. asthma), cardiovascular disorders (e.g. atherosclerosis), CC (e.g. infertility) and infectious disorders (e.g. inflammatory disorders (e.g. infertility) and infectious disorders (e.g. inflammatory disorders (e.g. infertility) and infectious disorders (e.g. inflammatory disorders compolitive) and infectious disorders (e.g. inflammatory disorders (e.g. inflammatory disorders compolitive) and infectious disorders (e.g. inflammatory disorders compolitive) and infectious disorders (e.g. inflammatory disorders compolitive) and infectious disorders (e.g. inflammatory disorders compolities of the invention can also be used in gene therapy.

CC AA$41685-AA$42192 represent DNA sequences encoding for the novel human componence and also the form nart of the printed componence and also the form nart of the printed componence and also the form nart of the printed componence and also the form nart of the printed componence and also the form nart of the printed componence and also the form nart of the printed componence and also the form nart of the printed componence and also the form nart of the printed componence and also the componence and also the componence and also the componence and also the componence and c
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05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-465566/50.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-JAN-2001; 2001US-0259678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID No 2049; 1180pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rosen CA, Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2209 BP; 629 A; 412 C; 442 G; 726 T; 0 other:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                  AAX90036;
  15-JUL-1999
                                                                                                                                                                          Fervidobacterium pennavorans; Ven 5; thermostable pullulanase; pulA;
                                                                                                                                                                                                                             Fervidobacterium pennavorans Ven 5 thermostable pullulanase DNA.
                                                                                                                                                                                                                                                                                  17-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                  AAX90036 standard; DNA; 2601 BP
                                                     W09935274-A2
                                                                                                     Fervidobacterium pennavorans
                                                                                                                                                        industrial saccharification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GCTTTCTTTGCCAAGAGCG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 72.5%; Score 17.4; DB 22; Length 2209; Local Similarity 94.7%; Pred. No. 1.4e+02;
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2000US-0256719.

2000US-0251479.

2000US-0251856.

2000US-0251868.

2000US-0251869.

2000US-0251869.

2000US-0251989.
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RESULT 9
AAK84218/c
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid encoding Fervidobacterium sp. Ven 5 thermostable pullulanase, useful for industrial saccharification processes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; AAY24380.
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                                                                   18-APR-2000;
19-MAY-2000;
07-JUN-2000;
28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
07-JUL-2000;
                                                                                                                                          24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                    AAK84218 standard; DNA; 36135 BP
                   14-JUL-2000;
26-JUL-2000;
26-JUL-2000;
                                                                                                                                                                                                                                                                                          Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                                                                                                        Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39030.
                                                                                                                                                                                                                                                                                                                                              07-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                 AAK84218;
                                                                                                                                                                                                              17-JAN-2001; 2001WO-US01354.
                                                                                                                                                                                                                                   09-AUG-2001.
                                                                                                                                                                                                                                                                        Homo sapiens.
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                                                 11-JUL-2000;
11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h 72.5%;
Similarity 94.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                  2000US-0186350.
2000US-0199874.
2000US-0199076.
2000US-0199123.
2000US-0209467.
2000US-0214886.
2000US-0214886.
2000US-0214886.
2000US-0214887.
2000US-0216847.
2000US-0217487.
2000US-0217487.
2000US-0218296.
2000US-0218296.
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                                                                                                                                                                       2000US-0180628.
2000US-0184664.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 17.4; DB 20;
Pred. No. 1.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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0;

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14-SEP-2000
21-SEP-2000
21-SEP-2000
25-SEP-2000
25-SEP-2000
25-SEP-2000
26-SEP-2000
27-SEP-2000
29-SEP-2000
29-SEP-2000
29-SEP-2000
29-SEP-2000
29-SEP-2000
29-SEP-2000
20-CCT-2000
02-CCT-2000
03-CCT-2000
03-NOV-2000
08-NOV-2000
08-NOV-2000
08-NOV-2000
08-NOV-2000
08-NOV-2000
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22-AUG-2000

22-AUG-2000

23-AUG-2000

30-AUG-2000

01-SEP-2000

01-SEP-2000

01-SEP-2000

01-SEP-2000

05-SEP-2000

06-SEP-2000

06-SEP-2000

06-SEP-2000

08-SEP-2000

08-SEP-2000
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        2000US-0240960
2000US-0241785
2000US-0241785
2000US-0241786
2000US-0241809
2000US-0241809
2000US-0241809
2000US-0246174
2000US-0246474
2000US-0246474
2000US-0246475
2000US-0246475
2000US-0246475
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2000US-0235836
2000US-0236327
2000US-0236367
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2000US-0236370
2000US-0237038
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2000US-0237038
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2000US-0237039
2000US-023937
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2000US-0232081
2000US-0231968
2000US-0232397
2000US-0232398
2000US-0232398
2000US-0232400
2000US-0232401
2000US-0233063
2000US-0233063
2000US-0233063
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2000US-023423
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2000US-0234288
2000US-0234988
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2000US-0231413.
2000US-0231414.
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17-NOV-2000
17-NOV-2000
17-NOV-2000
17-NOV-2000
17-NOV-2000
17-NOV-2000
01-DEC-2000
01-DEC-2000
05-DEC-2000
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17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
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17-NOV-2000;

17-NOV-2000;
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17-NOV-2000;
17-NOV-2000;
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2000US-0254097.
2001US-0259678.
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2000US-0246526
2000US-0246526
2000US-0246526
2000US-0246532
2000US-0246613
2000US-0246611
2000US-0246611
2000US-0246611
2000US-0249207
2000US-0249207
2000US-0249217
2000US-0249211
2000US-0249211
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2000US-0249211
2000US-0249212
2000US-0249213
2000US-0249214
2000US-0249215
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2000US-0249218
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2000US-0249218
2000US-0249218
2000US-0249284
2000US-0249284
2000US-0249286
2000US-0249286
2000US-0249288
2000US-0251868
                                                                                                                                                                                                           GENOME SCI INC
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Barash SC,

WPI; 2001-483426/52.

Nucleic acuseful for metastasis acids encoding ids encoding human immune/hematopoietic antigen polypeptides, preventing, diagnosing and/or treating cancers and

Disclosure; SEQ ID NO 39030; 3071pp + Sequence Listing; English

AKS4951 to AAK64702 encode the human immune/haematopoletic antigen (I) CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic cc activity, and can be used in gene therapy and vaccine production. (I) CC proteins and polynucleotides may be used in the prevention, diagnosis and creatment of diseases associated with inappropriate (I) expression. For CC example, they may be used to treat disorders associated with decreased that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) CC polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the CC diagnose and treat immune/haematopoletic-related diseases, especially cancers and cancer metastases of haematopoletic-derived cells. AAK64703 cc sequences from the present human immune/haematopoletic antigen genomic cc represent sequences used in the exemplification of the present invention.

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RESULT 10
ABV12459
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Matches
                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-MAR-2000;
25-MAY-2000;
09-JUN-2000;
18-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABV12459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABV12459 standard; cDNA; 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-FEB-2001; 2001WO-US05171.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200160860-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pharmacogenomic marker; gene; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human prostate expression marker cDNA 12450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-SEP-2002
                                                                                                                                                                                                                 The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate
                                                                                                                                                                                                                                                                                                                                               Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer stage of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-662795/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Schlegel R, Endege WO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-FEB-2000;
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                                                      Sequence 467 BP; 71 A; 115 C; 132 G; 149 T; 0 other;
                                                                                                                                                                                                                                                                                                                     Claim 1; Page 2053; 11750pp; English.
                                                                                                                                                                       (d) assessing the efficacy of a therapy for inhibiting prostate cancer
in a patient;
                                                                                                               (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                    cancer in a patient;
                                                                                                    patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Loca 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 CTTTCTTTGCCAAGAGC 18
             Local Similarity
                                                                                     is also useful as a pharmacodyanamic or pharmacogenomic marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prostate cancer; cytostatic; carcinogen; pharmacodyanamic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; 2000US-189862P.
; 2000US-207454P.
; 2000US-211314P.
; 2000US-219007P.
; 2000US-255281P.
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   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-183319P
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                90.0%;
                              70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Monahan JE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 17; DB 22; 1
Pred. No. 3.5e+02;
   0;
   Pred. No. 2.1); Mismatches
                             Score 16.8; DB 23;
                   2.1e+02;
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                                Length 467;
       Indels
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376 GCTTTCTTTGGCAAAAGCGC

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                            Matches
                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-MAR-2000;
25-MAY-2000;
09-JUN-2000;
18-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human prostate expression marker cDNA 33590
                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pharmacogenomic marker; gene; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABV33599;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200160860-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                             Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-FEB-2001; 2001WO-US05171
                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 7105; 11750pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schlegel R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       330
                                                                                sequence 506 BP; 80 A; 129 C; 145 G; 152 T; 0 other;
                                                                                                                                                                                              (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; \label{eq:cancer}
                                                                                                                                                                                                                            cancer in a patient;

    is also useful as a pharmacodyanamic or pharmacogenomic marker

                                                                                                                           patient;
                                                                                                                                                                                   (e)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Н
                                        Local Similarity
                                                                                                                                       selecting a composition for inhibiting prostate cancer in a patient; assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastasized in a patient; assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                   detecting presence of prostate cancer, stage of prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCTTTCTTTGGCAAAAGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCTTTCTTTGCCAAGAGCGC
GCTTTCTTTGCCAAGAGCGC 20
                            18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; 2000US-183319P.

2000US-189862P.

2000US-207454P.

2000US-211314P.

2000US-2119007P.

2000US-255281P.
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                            Conservative
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                                            90.0%;
                                                          70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Monahan JE;
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                             0;
                                                       score 16.8; DB 23; Length 506;
                               Score 10.0,
Pred. No. 2.1e+02;
Pred. No. 2:1e+02;
                                  Indels
                                  0,
                                  Gaps
                                     0;
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CC global changes in gene expression in tissues or cells exposed to the CC toxin and comparing these to gene expression in unexposed tissues or CC cells. Also included are methods of predicting at least one toxic ceffect of a compound or progression of a toxic effect, preferably the CC expression in a tissue or cell sample exposed to the compound of the compound of the compound of the compound of two or CC more genes listed in the specification, where differential expression of the genes is indicative of at least one toxic effect or progression. CC the method can also be used to identify an agent which modulates the compount in kit form), where each of the probes computed to support in kit form), where each of the probes comprises a sequence that system comprising at database containing information identifying the expression level in a tissue or cell sample exposed to a hepatotoxin of a conductivity in the expression level in a tissue or cell of a hepatotoxin of a conductivity in the specification. The method is useful for prediction of a compound conductivity in the specification. The method is useful for a least one gene changes in gene expression and for identifying to a the specification of a conductivity markers in drug screening and toxicity assays. The genes and conductivity markers in drug screening and toxicity assays. The genes and conductivity markers in drug screening and toxicity assays. The genes and conductivity and the specification of the physiological state of tissue or cell sequence is an expressed sequence tag (EST) or CDNA derived from a gene conductivity markers for the conductivity markers for the conductivity and derived from a gene conductivity and sequence is an expressed sequence tag (EST) or CDNA derived from a gene conductivity markers for the conductivit
              The invention relates to methods for predicting toxic effects of compounds or the progression of these toxic effects by determining the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Seq ID No 1639; 239pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Predicting toxic effects of compounds or the progression of these toxic effects by determining the changes in gene expression in tissues or cells exposed to the toxin and comparing these to gene expression in unexposed tissues or cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-241625/29.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GENE-) GENE LOGIC INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-JUN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rat; ss; hepatotoxin; expressed sequence tag; EST; drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           differential expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rat sequence differentially expressed in response to a hepatotoxin #1639.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABK63732 standard; cDNA; 1679 BP
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2001US-295798P.
2001US-297457P.
2001US-298884P.
2001US-303459P.
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2001US-290645P
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expressed sequence tag (EST) or cDNA derived from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Castle AL,
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                                                                                                                                                                     Query Match
                                                                                                                  Matches
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                                                                                                                                                                                                           Sequence 2304 BP; 541 A; 640 C; 721 G; 402 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                   useful in developmental biology and in elicidating cell signalling cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL101840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                  The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                   at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 3455; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cel
        226
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11-JUL-2000; 2000US-0614150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pharmaceutical; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-MAR-2002 (first entry)
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                                                                                                                                             TOCAT
                                                     4 TTCTTTGCCAAGAGCGCCGC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 TCTTTGCCTTGAGCGCCGCA 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ocal
TTCTTTGCCCAGAGCGCAGC 245
                                                                                                                  18;
                                                                                                                                          Similarity
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                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adams M,
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                                                                                                                              70.0%;
90.0%;
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                                                                                                             0
                                                                                                                                                   Score 16.8; DB 23; Length 2304;
                                                                                                                                    Pred
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                                                                                                          Mismatches
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                                                                                                                              No
                                                                                                                        2.7e+02;
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                                                                                                       Indels
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RESULT 14
ABL02990
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                                                                                                                                                                             RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pharmaceutical; gene; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                               capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL101840-ABL16175) and the encoded proteins `
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 3452; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; ABB58887.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                    The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                          Sequence 4446 BP; 1191 A; 1023 C; 1084 G; 1148 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated nucleic acid detection reagent
altered culture condition; environmental stress; physiological provocation; ds.
                            Differential gene expression; genomic sequenced tag; GST;
                                                        Bacillus clausii genomic sequence tag (GST) #3572.
                                                                                                                                                 ABK80729 standard; DNA; 408
                                                                                                                                                                                                                                                                                                                                                                        at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                    (ABB57737-ABB72072)
                                                                                         13-AUG-2002
                                                                                                                                                                                                                         613 TTCTTTGCCCAGAGCGCAGC 632
                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                         4 TTCTTTGCCAAGAGCGCCGC 23
                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Adams M,
                                                                                                                                                                                                                                                                                   Conservative
                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                 70.0%; Score 16.8; 90.0%; Pred. No. 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Li PWD,
                                                                                                                                                                                                                                                                                      0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Myers EW;
                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                   3e+02;
                                                                                                                                                                                                                                                                                                                      DB 23;
                                                                                                                                                                                                                                                                                        2;
                                                                                                                                                                                                                                                                                                                    Length 4446;
                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                           0;
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В

374 GCATTCTTGCCCAAGTGCGCCGC 396

0,

Search completed: March 17, 2003, 10:50:45

time

: 146.715 secs

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The invention describes a method of monitoring differential expression of CC genes in a first Bacillus cell relative to expression of the genes in CC other Bacillus cells, comprising hybridising labelled nucleic acid probes CC isolated from Bacillus cells to a substrate containing array of Bacillus CC isolated from Bacillus cells to a substrate containing array of Bacillus CC genomic sequenced tags (GST), examining the array, and determining CC expression by an observed hybridisation reporter signal of CC a spot in the array. The method is useful for measuring the expression of cell relative to expression of the same genes CC in one or more second Bacillus cells. The method is useful for monitoring cell expression of several genes from a Bacillus cell, discovering new CC global expression of several genes from a Bacillus cell, discovering new CC genes, identifying possible functions of unknown open reading frames and CC monitoring gene copy number variation and stability. Monitoring changes compitoring gene copy number variation and stability monitoring changes in expression of genes may be used to provide a representation of the way cells adapt to changes in culture conditions.

CC in which Bacillus cells adapt to changes in culture conditions of the value of the provide and array cells one gene or one open reading frame, since sequence information is cavellable. This sequence represents a genomic sequence tag (GST) used in the provide a provide and the conditions of the condition
                                                        Matches
                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-OCT-2000; 2000US-0680598.
27-MAR-2001; 2001US-279526P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-OCT-2001; 2001WO-US31437.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-APR-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus clausii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 11; SEQ ID NO 8020; 200pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequenced tag array
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacillus cells, by using substrate containing Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Monitoring differential expression of several genes in first Bacillus cell relative to expression of same genes in one or more second
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-416684/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (NOVO)
                                                                                                                                                                                                                                                                 the method of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (NOVO ) NOVOZYMES BIOTECH INC
                                                                                                                                                        Sequence 408 BP; 106 A; 86 C; 104 G; 111 T; 1 other;
                                                                                                                                                                                                           ftp.wipo.int/pub/published_pct_sequences.
                                                                                 Local
1 GCTTTCTTTGCCAAGAGCGCCGC 23
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                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clausen IG;
                                                           Conservative
                                                                               69.2%; Score 16.6; DB 24
82.6%; Pred. No. 2.5e+02;
                                                              0;
                                                                 Mismatches
                                                                                                                 DB 24; Length 408;
                                                                   Indels
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                                                                      0;
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Title:
Perfect score:
Sequence:
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Maximum DB seq length: 2000000000
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                   Database
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                      16154066 seqs, 8097743376 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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24
1 gctttctttgccaagagcgccgca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     March 17, 2003, 10:23:12; Search time 848.387 Seconds (without alignments) 458.154 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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gb_est2: *
gb_htc: *
gb_est3: *
gb_est4: *
gb_est5: *
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em_estov: *
em_estpl: *
em_estro: *
em_htc: *
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                                                   em_gss_mus:*
em_gss_other:*
em_gss_pro:*
em_gss_rod:*
                                                                                                                  em_gss_hum:*
em_gss_inv:*
em_gss_pin:*
em_gss_vrt:*
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533 533 544 5544 575 5762 5762 5778 5778 5778 5778 5778 5778 5778 577	
111944444444444444444444444444444444444	99 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 114 / 1
BOG538268 BOG549241 BOG536918 BOG536918 BOG536602 BOG536602 BOG536602 BOG536602 BOG53602 BMG85757 BMG85912 BOG537208 BOG639291 BOG538291 BOG538291 BOG538291 BOG538291 BOG538291 BOG538291 BOG538291 BOG538291 BOG538291 BOG538291 BOG538291 BOG538291 BOG538291 BOG538291 BOG538291 BOG538291	AL712412 BM666193 BM688227 AL712402 BQ250368 BM682069 BM6629137 BM690137 BM690137 BM690311 BQ640665 BQ638862 BM6937734 BM6937734 BM6937734 BM6937734 BM69319 BM69319 BM69319 BM69319 BM69319 BM69319
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### ALIGNMENTS

RESULT 1

	JOURNAL MEDLINE COMMENT	REFERENCE AUTHORS TITLE	ACCESSION VERSION KEYWORDS SOURCE	BM694379 LOCUS DEFINITION
451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250 Fax: 319 335 9565 Email: msoares@blue.weeg.uiowa.edu Tissue Procurement: Dr. Gregg Hageman Tissue Procurement: Dr. M. Bento Soares, Univeristy of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa	Genome Res. 6 (9), 791-806 (1996) 97044477 Contact: Soares, MB Program for Rat Gene Discovery and Mapping University of Iowa	Homo Sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.  1 (bases 1 to 303) Bonaldo, M.F., Lennon, G. and Soares, M.B. Normalization and subtraction: two approaches to facilitate gene	BM694379 GI:19007637 EST. human.	BM694379 UI-E-CI1-afp-p-18-0-UI.rl UI-E-CI1 Homo saplens cDNA clone UI-E-CT1-afp-p-18-0-UI 5', mRNA sequence.

Result No.

Score

Query Match

Length

В

IJ

Description

SUMMARIES

a

89.2 89.2 89.2 89.2

303 319 337 340 349 441

14

BM694379 BQ637565 BM723222 BM682444 BM703950 BM690151

BM694379 UI-E-CI1-BQ637565 hellg04.y BM72322 UI-E-EJ0-BM682444 UII-E-CI0-BM703950 UI-E-CK1-BM690151 UI-E-CL0-

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ACCESSION
VERSION
                                                                                                                FEATURES
                                                                                                                                                                                                                                                                                                                                                                      COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity hes 22; Conserv
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                                                                                                                                                                                                                                                                                                                                                                               Wistow,G., Bernstein,S.L., Wyatt,M.K., Ray,S., Behal,A., Touchman J.W., Bouffard,G., Smith,D. and Peterson,K. Expressed sequence tag analysis of human retina for the NEIBank Project: Retbindin, an abundant, novel retinal cDNA and alternative splicing of other retina-preferred gene transcripts Mol. Vis. 8 (4), (2002) In press
                                                                                                                                                                 Email: graeme@helix.nih.gov
Plate: 11 row: g column:
                                                                                                                                                                                                                        Tel: 301 402 3452
Fax: 301 496 0078
                                                                                                                                                                                                                                                                                                         Section on Molecular Structure and Function National Eye Institute
                                                                                                                                                                                                                                                                                                                                                                Contact: Wistow G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BQ637565 319 bp mRNA linear EST 15-JUL-2(hell904.yl Human Retina cDNA (Un-normalized, unamplified): hd/he Homo_sapiens cDNA clone hell904 5', mRNA sequence.
                                                                                                                                    Seq primer: M13RP1 reverse primer (ABI).
                                                                                                                                                                                                                                                                         6/331, NIH, Bethesda, MD 20892-2740, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genetics (www.resgen.com).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clone Distribution: Researchers may obtain clones from Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 319)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70 a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="DHIOB (Life Technologies) (TI phage resistant)"
/lab_host="DHIOB (Life Technologies) (TI phage resistant)"
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: Ecor I; Site_2: Not I;
UI-E-CII is a normalized cDNA library containing the
following tissue(s): RPE and Choroid. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT7T3-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is ACCTA.
This library was created for the program, Gene Discovery
in the Visual Sustema Supported he was found to the
/db_xref="taxon:9606"
/clone="hellg04"
                                                      /organism="Homo sapiens"
                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in the Visual System, supported by National Eye Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="RPE and Choroid"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="UI-E-CI1-afp-p-18-0-UI"
/clone_lib="UI-E-CI1"
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95.7%;
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Pred. No. 23
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Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                   Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
                                                                                                                                                                                                                                                             The following repetitive elements were found in this cDNA sequence: 295-332, >AT_rich#Low_complexity (matched compliment) Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                            Genetics (www.resgen.com).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 319 335 8250 Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Soares, {\tt MB} Program for Rat Gene Discovery and Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97044477
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337 bp mRNA linear EST 01
UI-E-EJU-aio-i-15-0-UI.rl UI-E-EJU Homo sapiens cDNA clone
UI-E-EJU-aio-i-15-0-UI 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 337)
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/tissue_type="fetal eyes, lens, eye anterior segment,
optic nerve, retina, Retina Foveal and Macular, RPE a
                                                                     /clone="UI-E-EJO-aio-i-15-0-UI"
/clone_lib="UI-E-EJO"
                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab_host="EMDH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="Retina"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Medical Research Building Iowa City, IA 52242, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89.2%;
95.7%;
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Pred. No. 23;
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REFERENCE

AUTHORS

JOURNAL TITLE SOURCE KEYWORDS VERSION ACCESSION

ORGANISM

RESULT 3 BM723222

B

ORIGIN BASE COUNT

Matches

DEFINITION

Locus

FEATURES

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RESULT 4
BM682444/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                                                                                                                                                                                          Email: msoares@blue.weeg.ulowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
                                                                                                                                                                                                                                                                     Genetics (www.resgen.com).

The following repetitive elements were found in this cDNA sequence: 1-37, >AT_rightLow_complexity (matched compliment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 340)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
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                                                                                                                                                                                                                              POLYA-Yes.
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                                                                                                                                                                                                                                                           Seq primer: M13 Forward
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/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/note="Organ: eye; Vector: py773-Pac (Pharmacla) with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
UT-E-EJO is a subtracted cDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into py773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT), B tail. The sequence tags for this library are: fetal eyes, AGAATCAAGA; lens, CGATTAGCGA; eye anterior segment, AARGCGCAT; oppilc nerve, CCATTAAGTG; retina, CCGCG; Retina Foveal and Macular, GTCC; RPE and Chorold, ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                       /clone="UI-E-EJO-aio-i-15-0-UI"
/clone_lib="UI-E-EJO"
/tissue_type="fetal eyes, lens, eye anterior segment,
                                                                                                     /db_xref="taxon:9606"
                                                                                                                               organism-"Homo sapiens"
                                                                                                                                                                                             Location/Qualifiers
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95.7%;
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Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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KEYWORDS SOURCE ORGANISM

VERSION ACCESSION DEFINITION

REFERENCE

AUTHORS

밁

Matches

BASE COUNT

MEDLINE COMMENT

REFERENCE AUTHORS

VERSION KEYWORDS

ACCESSION DEFINITION

SOURCE

ORGANISM

RESULT 5 BM703950

POCAR

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ORIGIN

COMMENT

JOURNAL TITLE

FEATURES

/clone="UI-E-CK1-afk-m-09-0-UI"

JOURNAL TITLE

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BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                  Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                        Genetics (www.resgen.com).
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                         Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BM703950
349 bp mRNA linear EST 28
UI-E-CK1-afk-m-09-0-UI.rl UI-E-CK1 Homo sapiens cDNA clone
UI-E-CK1-afk-m-09-0-UI 5', mRNA sequence.
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Bonaldo, M.F., Lennor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                          cDNA Library preparation: Ďr. M. Bento Soares, Univeristy of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa Clone Distribution: Researchers may obtain clones from Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genome Res. 6 (9), 791-806 (1996)
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/note="Organ: eye; Vector: pT773-Pac (Pharmacia) with a
modified polylinker: Site_1: Ecor I: Site_2: Not I:
UI-E-EJO is a subtracted cDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT773-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tags for this library are: fetal eyes, AGAATCAAGA
; lens, CGATTAGCGA; eye anterlor segment, AATGCCCCAT;
optic nerve, CCATTAGTG; retina, CGCG; Retina Foveal and
Macular, GTCC; RPE and Choroid, ACCTA. This library was
created for the program, Gene Discovery in the Visual
System, supported by National Eye Institute (NEI).
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                          Location/Qualifiers
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76 c 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="fetal and adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89.2%;
95.7%;
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DEFINITION
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BM690151 441 bp mRNA linear FUI-E-CLO-acd-f-11-0-UI.rl UI-E-CLO Homo sapiens cDNA UI-E-CLO-acd-f-11-0-UI 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                    Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Seguencing by: Dr. M. Bento Soares, Univeristy of Iowa
                                                                                                                                                                                                                                                             Genetics (www.resgen.com).
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         University of Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Program for Rat Gene Discovery and Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Soares, MB
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/lab host="PHIOB (Life Technologies) (T1 phage resistant)"
/lab host="PHIOB (Life Technologies) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-E-CRI is a normalized cDNA library containing the
following tissue(s): Retina Foveal and Macular. The
library was constructed according to Bonaldo, Lennon and
Soares, Genome Research, 6:791-806, 1996. First strand
cDNA synthesis was primed with an oligo-dT primer
containing a Not I site. Double stranded cDNA was ligated
to an EcoR I adaptor, digested with Not I, and cloned
directionally into pTTT3-Pac vector. The oligonucleotide
used to prime the synthesis of first-strand cDNA contains
a library tag sequence that is located between the Not I
site and the (dT).8 tail. The sequence tag for this
library is GTCC. This library was created for the program,
Gene Discovery in the Visual System, supported by National
Eye Institute (NEI)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="UI-E-CLO"
/clone_lib="UI-E-CLO"
/tissue_type="human retina"
/dev_stage="adult"
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/tissue_type="Retina Foveal and Macular"
/dev_stage="adult"
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/lab_host-"DH10B (Life Technologies) (T1 phage resistant)"
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95.7%;
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Pred. No. 24;
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ACCESSION

KEYWORDS VERSION BM690151 RESULT

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Matches

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RESULT 7
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                       Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s. wiemann@dkfz- heidelberg.de;
sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing
consortium of the German Genome Project.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wambutt,R., Heubner,D., Mewes,W., Weil,B. and Wiemann,S.
EST (Wambutt,R., Heubner,D., Mewes,H.W., Weil,B. and Wiemann,S.)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DKFZp68601888_r1 686 (synonym: h
DKFZp68601888 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 442)
                                                                                                                                                                                                                                                                                                                                                                                               Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This clone (DKFZp68601888) is available at the RZPD in Berlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               No s1 sequence available
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Wambutt R
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                         Similarity
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                                                                                                                            106 a
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Conservative
                                                                                                                                              /lab_host="DH10B"
/note="Vector: pTriplEx2; Site_1: SfiIA; Site_2: SfiIB; cDNA-collection"
                                                                                                                                                                                                                                                                     /clone_"DKFZp68601888"
/clone_lib="686 (synonym: hlcc3)"
                                                                                                                                                                                                                         /tissue_type="human skeletal muscle"
/dev_stage="adult"
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/db_xref="taxon:9606"
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95.7%;
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Pred. No. 26;
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                                                      Length 442;
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BM696193
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226 GCGTTCTTTGCCAAGAGCGCCGC 248
                                            1 GCTTTCTTTGCCAAGAGCGCCGC 23
                                                                                                                            Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: M13 Reverse
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1 (bases 1 to 446)
Bonaldo, M. F., Lennon, G. and Soares, M.B.
                                                                                                                            Similarity
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UI-E-CL1-afa-d-24-0-UI.rl UI-E-CL1 Homo sapiens cDNA clone
UI-E-CL1-afa-d-24-0-UI 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Soares, MB
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                                                                                                  Conservative
                                                                                                                                                                                                  //lab_host="blidde" (Life Technologies) (T1 phage resistant)"
//lab_host="blidde" (Life Technologies) (T1 phage resistant)"
//lab_host="blidde" (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI = C(LI is a normalized cDNA library containing the following tissue(s): retina. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is sequence tag for this library is CCGCG. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="human retina"
/dev_stage="adult"
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/clone_lib="UI-E-CL1"
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/db_xref="taxon:9606"
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                                                                                                                       89.2%;
95.7%;
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                                                                                                                    Score 21.4;
Pred. No. 26;
                                                                                             Mismatches
                                                                                                                                      DB 14; Length 446;
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BM688227
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82 GCGTTCTTTGCCAAGAGCGCCGC 104
                                                                                                                               Local
                                                 1 GCTTTCTTTGCCAAGAGCGCCGC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: msoares@blue.weeg.ulowa.edu
Tlssue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genetics (www.resgen.com).
The following repetitive elements were found in this cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        451 Eckstein Medical Research Building Towa City, IA 52242, USA Tel: 319 335 8250 Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq primer: M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence: 425-459, >AT_rich#Low_complexity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UI-E-CLO-aby-g-03-0-UI.rl UI-E-CLO Homo sapiens cDNA clone UI-E-CLO-aby-g-03-0-UI 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Soares, MB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genome Res. 6 (9), 791-806 (1996)
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                                                                                                                                                                                                     /lab_host="Discrete" (TI phage resistant)"
//ab_host="Discrete" (Vector: pT7T3-Pac (Pharmacla) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; UI-E-CLO is a cDNA library containing the following tissue(s): retina. The library containing the following to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-df primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is sequence tag for this library is CCGCG. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."
                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="human retina"
/dev_stage="adult"
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/clone_lib="UI-E-CL0"
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95.7%;
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                                                                                                0; Mismatches
                                                                                                                         Score 21.4;
Pred. No. 27
                                                                                                                                            DB 14;
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                                                                                                Indels
                                                                                                                                            Length 469;
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Wambutt,R., Heubner,D., Mewes,W., Weil,B. and Wiemann,S.
EST (Wambutt,R., Heubner,D., Mewes,H.W., Weil,B. and Wiemann,S.)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DKFZp686N1788_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
DKFZp686N1788 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de; sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This clone (DKFZp686N1788) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 1405 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                TaE25006AllR TaE25 Triticum aestivum cDNA clone TaE25006AllR, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       No s1 sequence available
                                                                                                       Cereal Research Centre, Agriculture and Agri-food Canada
195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9
                                                                                                                                                       Unpublished (2002)
Contact: Dr. Sylvie Cloutier
                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldea; Triticeae; Triticeum.
                                                                                                                                                                                                                                                                                                                               Triticum aestivum
was cloned directionally, not all sequences generated with reverse primer were from the 5' end (same with forward primer and 3' end).
                                                Email: scloutier@em.agr.ca
                                                                                                                                                                                                 Wheat functional genomics - Glenlea developing seeds cDNA libraries
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                                                                (204) 983-2340
(204) 983-4604
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/note="Vector: pTriplEx2; Site_1: SfiIA; Site_2: SfiIB; cDNA-collection"
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/clone_lib="686 (synonym: hlcc3)"
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/dev_stage="adult"
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/db_xref="taxon:9606"
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95.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      174 GCGTTCTTTGCCAAGAGCGCCGC 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GCTTTCTTTGCCAAGAGCGCCGC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plate: 006 row: A colused primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               l Similarity
22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Average insert size is >870 bp plate: 006 row: A column: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BM688069 474 bp mRNA linear EST 28 UI-E-CLO-aby-c-04-0-UI.rl UI-E-CLO Homo saplens cDNA clone UI-E-CLO-aby-c-04-0-UI 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                       Tissue Procurement: Dr. Gregg Hageman cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa DNA Sequencing to: M. Bento Soares, Univeristy of Iowa Clone Distribution: Researchers may obtain clones from Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242,
                                                                                                                                                                                                                                               The following repetitive elements were found in this cDNA sequence: 335-367, >AT_rich#Low_complexity Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Soares, MB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97044477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bonaldo, M.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BM688069.1 GI:19001327
                                                                                                                                                                                                                                                                                                                         Genetics (www.resgen.com).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: msoares@blue.weeg.uiowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 319 335 8250 Fax: 319 335 9565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pCMV-SPORT6.0 (invitrogen Technologies);
Site_1: NotI; Site_2: MluI; mRNA obtained from wheat seeds
of cultivar Glenlea 25 days post-anthesis"
a 164 c 108 g 91 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="developing seeds"
/dev_stage="25 days after anthesis"
/lab_host="E. coli DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="TaE25006A11R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cultivar="Glenlea"
/db_xref="taxon:4565"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Triticum aestivum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="TaE25"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
/dev_stage="adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/lab_nost="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
                                                                                                                /clone="UI-E-CL0-abv-c-04-0-UI"
/clone_lib="UI-E-CL0"
                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                Location/Qualifiers
                                                                                        /tissue_type="human retina"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 to 474)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               164 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89.2%;
95.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lennon, G. and Soares, M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 21.4;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST 28-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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RESULT 13
BM662914/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
7el: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41 GCGTTCTTTGCCAAGAGCGCCGC 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: M13 Forward POLYA-Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 478)

Bonaldo, M.F., Lennon, G. and Soares, M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BM662914 478 bp mRNA linear EUI-E-CKO-aan-e-04-0-UI.Sl UI-E-CKO Homo sapiens cDNA UI-E-CKO-aan-e-04-0-UI 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Res. 6 (9), 791-806 (1996)
/dev_stage*adult*
/lab_host="DH10B (Life Technologies) (T1 phage resistant)*
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-E-CKO is a cDNA library containing the following
tissue(s): Retina Foveal and Macular. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xxef="taxon:9606"
/clone="UI-E-CKO-aan-e-04-0-UI"
/clone_11b="UI-E-CKO"
                                                                                                                                                                                                                                                           /tissue_type="Retina Foveal and Macular"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89.2%;
95.7%;
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Pred. No. 2
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REFERENCE

TITLE

SOURCE KEYWORDS VERSION ACCESSION DEFINITION

ORGANISM

ORIGIN BASE COUNT

ORIGIN

Matches

COMMENT

COMMENT

JOURNAL TITLE AUTHORS

REFERENCE

KEYWORDS VERSION ACCESSION DEFINITION BM690137 RESULT 14

ORGANISM

JOURNAL MEDLINE

FEATURES

source

FEATURES

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BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: msoares@blue.weeg.ulowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence: 425-459, >AT_rich#Low_complexity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BM690137 493 bp mRNA linear EST 28 UT-E-CLO-acd-d-08-0-UI.rl UI-E-CLO Homo sapiens cDNA clone UI-E-CLO-acd-d-08-0-UI 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bonaldo, M.F., Lennon, G. and Soares, M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   The following repetitive elements were found in this cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 493)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BM690137.1 GI:19003395
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/lab_host="DHIOB (Life Technologies) (T1 phage resistant)"
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-E-CLO is a cDNA library containing the following
tissue(s): retina. The library was constructed according
to Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
                                                                                                                                                                                /tissue_type="human retina"
/dev_stage="adult"
                                                                                                                                                                                                                                        /db_xref="taxon:9606"
/clone="UI-E-CLO-acd-d-08-0-UI"
/clone_lib="UI-E-CLO"
                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAG_LIB-UI-E-CKO
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                                                                                                                                                                                                                                                                                                                                                           . 493
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Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        123 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST 28-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
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Query Match
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UI-E-CI1-abh-c-07-0-UI.rl UI-E-CI1 Homo sapiens cDNA clone
UI-E-CI1-abh-c-07-0-UI 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 493)
Bonaldo, M. F., Lennon, G. and Soares, M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genetics (www.resgen.com).
The following repetitive elements were found in this cDNA sequence: 302-335, AT_rich#Low_complexity
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hayeman
cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome Res. 6 (9), 791-806 (1996)
97044477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BM691592.1 GI:19004850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  110 a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an ECOR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CCGCG. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        319 335 9565
                                                              /db_xref="taxon:9666"
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/tissue_type="RPE and Choroid"
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/lab_host="DH10B (Life Technologies) (T2 phage resistant)"
/lab_host="Roran: eye; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-E-CII is a normalized Chan Library containing the
following tissue(s): RFE and Choroid. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First Strand CDNA
Genome Research, 6:791-806, 1996. First Strand CDNA
synthesis was primed with an oligo-dT primer containing Not I site. Double stranded cDNA was ligated to an EcoR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 27;
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 14; Length 493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST 28-FEB-2002
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REFERENCE

AUTHORS

TITLE

JOURNAL

SOURCE KEYWORDS VERSION ACCESSION

ORGANISM

COMMENT

FEATURES

source

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116 a
                                                                                            adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is ACCTA. This library was created for the program, Gene Discovery this library was created for the program.
                             (NEI)
                                                           the Visual System, supported by National Eye Institute
157 c
111 g
           109 t
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BASE COUNT Query Match 89.2%; 95.7%; Score 21.4; Pred. No. 27 DB 14; Length 493;

Matches

Best Local Similarity

Conservative

0; Mismatches

Indels

0 Gaps

0;

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Matches

DEFINITION BM691592

RESULT 15

BASE COUNT

Search completed: March 17, 2003, 13:09:15 Job time: 851.387 secs

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Minimum I
Maximum I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq length: 2000000000
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                                                                              IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           March 17, 2003, 09:43:42; Search time 202.495 Seconds (without alignments) 3161.870 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2054640 seqs, 14551402878 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-836-439-4
22
                                                                                                                                                                                                                                                                                                                                                                                                                              Maximum Match 100%
Listing first 45 summaries
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gb_ph: *
gb_pr: *
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Pred. ŏ. 18 the number of results predicted by chance to have

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

#### Result ð Score 20 20 20 20 19 19 19 19 Match Length Query 118795 119767 1180638 201481 201486 214889 274349 112952 22499 22495 22495 22495 22495 63484 63484 63484 63484 1113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 11395 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 11395 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 113955 1139 133095 152147 DB SCYPIL252C SCYPIL252C SCYPIL253C SC38KCXVI CBRC46G14 ACL109155 AC130126 AC130126 AC131126 AC139147 AC092031 AL139147 AC095684 AC068291 AC095487 AC004841 AF112374 AF005448 AC0111035 AC019195 AC093799 AC068236 AC113076 AC068236 AC113076 AC0682370 AC068270 AC093623 AP005572 AC117913 AC113320 AC069223 AC068763 AC027080 AC027080 AC130437 AC022912 AC046146 AC095531 AF012746 AL139147 Human DNA AC092031 Homo sapi AL137158 Homo sapi AC068291 Homo sapi AC095684 Rattus no AP005487 Oryza sat AC004841 Homo sapi AF112374 Danio rer AL845428 Danio rer Z73608 S.cerevisia Z73609 S.cerevisia Z67751 S.cerevisia AC091216 Caenorhab AC109155 Mus muscu AC130512 Rattus no AC108916 Mus muscu AC131268 Homo sapi AC131262 Rattus no AC069223 Homo sapi AC068763 Homo sapi AC027080 Homo sapi AC130437 Homo sapi AC022912 Homo sapi AC022912 Homo sapi AC093623 Homo sapi AP005572 Oryza sat AF012746 Danio rer Z73608 S.cerevisia AL359074 Human DNA AC019195 Homo sapi AC068389 Homo sapi AC095531 Rattus no AC117913 Rattus no AC113320 Mus muscu AC046146 Description 35 Mus muscu 5 Rattus Homo sapi Homo sapi Rattus no Homo sapi Rattus no Rattus no Homo sapi Oryza sat Mus muscu Human chr Mus muscu

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KEYWORDS SOURCE ORGANISM RESULT 1 AC046146 LOCUS REFERENCE VERSION ACCESSION DEFINITION AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 13095)
Metzker, M. L., Lewis, L. R., Hume, J., Edwards, C., Harris, C., Dederich, D., Thomas, S., Okwuonu, G., Carlock, C., Garner, T., Mus musculus. AC046146 AC046146.6 GI:16118085 HTG; HTGS_PHASE1. ACO46146

133095 bp DNA linear HTG 16-OCT-2001
MUS musculus chromosome 12 clone RP23-321N21, *** SEQUENCING IN
PROGRESS ***, 31 unordered pieces. AC046146

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ALIGNMENTS

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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Addison, S., Pace, A., Williams, G., Bonnin, D., Brooks, A., Brown, J., Buhay, C., Bunac, C., Burkett, C., Chacko, J., Chen, G., Chen, Z., Cox, C., Davis, C., Delgado, O., Ding, Y., Dugan-Rocha, S., Fernandez, C., Ferraguto, D., Forcoun-Tansey, J., Gill, R., Gorrell, J.H., Gunaratne, P., Haller, G., Hernandez, J., Hogues, M., Hosak, H., Hou, X., Huber, J., Jackson, L., Jia, Y., Kelly, J., Kelly, S., Koyar, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Martin, R., Koyar, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Martin, R., Massey, E., McLeod, M.P., Mei, G., Moore, S., Morgan, M., Morris, S., Neal, D., Nelson, A., Nguyen, N., Oguh, M., Parish, B., Perez, L., Reiter, D., Say, J., Shen, H., Vasquez, L., Wallington, S., Milliamson, A., Wrensford, G., Zhou, X., Bouck, J., Hodgson, A., Muzny, D. M., Rives, M., Scherer, S., Sodergren, E., Weinstock, G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (13-APR-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Oct 14, 2001 this sequence version replaced gi:11094634.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Worley, K. and Gibbs, R. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 31 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                      as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequencing vector: Mi3; L08621
Chemistry: Dye-primer Bodipy: 94% of reads
Chemistry: Dye-terminator Big Dye: 6% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 118378 bases at least Q40
Consensus quality: 118476 bases at least Q30
Consensus quality: 155160 bases at least Q20
Estimated insert size: 148882; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center project Information Center project name: MADV Center clone name: RP23-321N21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center code: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Baylor College of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality coverage: 2.1x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                        10337
10437
19209
19309
26725
26825
33513
33613
39389
      39489
45331
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50899
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45430
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COMMENT

TITLE

TITLE

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RESULT 2
AC095531
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          REFERENCE
                                                             SOURCE
                                                                                                                 DEFINITION
                                                                                                                                                                             Db 71615 AAGACAAAATCTAGACAAGCAA 71636
                                                                                                                                                                                                                                                              ORIGIN
                                                                                                                                                                                                                                                                         BASE COUNT
                                                                                                                           LOCUS
                                                                       KEYWORDS
                                                                                  VERSION
                                                                                            ACCESSION
                                                                                                                                                                                                                      Matches
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                                                  ORGANISM
AUTHORS
                                                                                                                                                                                                                                                                                                                            source
                                                                                                                                                                                                 1 AAGAAAAATCTAGACAAGCAA 22
                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                       21;
                                                                                                  Rattus norvegicus clone CH230-8N2, 58 unordered pieces.
                                                  Rattus norvegicus
                                                                                           AC095531
Muzny, D.M., Adams, C., Adio-Oduola, B.,
                                                                       HTG; HTGS_PHASE1.
                                                                                  AC095531.3 GI:21716992
                                                                                                                           AC095531
                    Rattus.
                              Mammalia; Eutheria;
                                        Eukaryota; Metazoa;
                                                              Norway
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30809 c 29300 g
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/chromosome="12"
                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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107955: contig
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                              Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae;
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consists of 58 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence

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Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,
Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Lowis, L.C.,
Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.,
Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H.,
Lozado, R.J., Lu, X., Lucler, A., Lucler, R., Luna, R., Ma, J.,
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Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G.,
Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I.,
Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H.,
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Sutton, A., Ward-Moore, S., Warren, R., Washington, C., Watlington, S.,
Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S.,
Weinstock, G. and Gibbs, R.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., David, R., L., David, C., Davila, M.L., David, G., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwalte, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Falls, T., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, K., Harris, K., Harlak, P., Hawes, A., Hernandez, J., Holds, F., Howard, S., Huber, J., Halloway, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Huly, S., Hume, J., Jackson, L.E., Jacobson, B. Tia, V., Thomson, B. Tolling, S., Tol
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Direct Submission

Submitted (17-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 152147)
* NOTE: Estimated insert size may differ from sequence length 
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (10-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 9, 2002 this sequence version replaced gi:17942049.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T. Barbarla, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Barbarla, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.F. Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, R., Chen, Z., Chavazos, S.R., Chacko, J., Chavazos, Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, R., Chen, Z., Chowdhry, J., Christopoulos, C., Chen, Z., Chowdhry, J., Chowdhry, J., Christopoulos, C., Chen, Z., Chowdhry, C., Chowdhry, C., Chen, Z., Chowdhry, C., Chen, Z., Chowdhry, J., Christopoulos, C., Chen, Z., Chowdhry, C., Chen, Z., Chowdhry, C., Chen, Z., Chowdhry, C., Chowdhry, C., Chen, Z., Chowdhry, C., Chowdhry, C., Chen, Z., Chowdhry, C., Chen, Z., Chowdhry, C., Chowdhry, C., Chen, Z., Chowdhry, C., Chen, Z., Chowdhry, C., Chowdhry, C., Chowdhry, C., Chen, Z., Chowdhry, C., Chen, Z., Chowdhry, C., Chowdhry, C.,
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                                                                                                                                                                                                                                                                                                                               Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap: version 0.990329
Consensus quality: 92864 bases at least Q40
Consensus quality: 97631 bases at least Q30
Consensus quality: 101839 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Center project Information
Center project name: GCPY
Center clone name: GCP30-8N2
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REFERENCE AUTHORS TITLE

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COMMENT

JOURNAL REFERENCE AUTHORS

TITLE JOURNAL

as soon as it is available and the accession number will be preserved. 44293 44393 46709 46809 49243 49343 51259 53361 53361 33408 35427 35527 36881 36981 38530 38530 40147 40247 42518 31410 31510 33308 27940 28040 29821 29921 24020 25189 20846 20946 22784 22784 22884 23920 gap of contig gap of gap of contig contig gap of contig gap of contig of 1688 unknown of 1916 of 2434 of 2316 of 2271 unknown of 1517 unknown of 2019 unknown of 1798 unknown of 1489 of 1781 unknown of 1838 unknown of 1341 of 1579 unknown of 1937 of 1152 of 1267 of 2002 of 1675 of 1549 of 1354 unknown of 1405 unknown of 1146 of 1169 of 1036 unknown of 1413 unknown of 1788 unknown of 1232 unknown of 1160 of 1117 unknown of 1438 unknown of 1516 unknown of 1454 unknown of 1151 bp in length unknown unknown unknown unknown unknown unknown length bp in . length bp in ] ni dq bp in length ength ength ength 'n length length length length length length length length length length

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                           Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C. Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chacko, J., Ch
                                                                                                                                                                                                                                                                                                                             AC117913 172497 bp DNA linear HTG 18-JUL-Rattus norvegicus clone CH230-35D24, *** SEQUENCING IN PROGRESS
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                                                                                                                                                                                                                   Norway rat.
Rattus norvegicus
                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                         HTG; HTGS_PHASE1.
                                                                                                                                                                 Rattus
                                                                                                                                                                                                                                                                           AC117913.4 GI:21747159
                                                                                                                                               l (bases 1 to 172497)
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Chen,R., Chen,Z., Chowdhry,I., Christopou
d,C.D., Cox,C., Coyle,M.D., Dathorne,S.R.,
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                                                                                                        Banks, T.,
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                                                                                                                            Allen, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,
Homsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.
Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H.,
Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
Maheshwari,M., Meidor,M., Meidor,M., Mei,G., Metzker,M.,
Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,
Moser,M., Neal,D., Newtson,J., Newtson,N., Nguyen,A., Nguyen,N.,
Nguyen,N., Nickerson,E., Nwokenkwo,S., Ogah,M., Okwuonu,G.,
Oragunye,N., Oviedo,R., Partmus,E., Pu,L.L., Quiles,M., Ren,Y.,
Rives,M., Rojas,A., Rojubokan,L., Rolfe,M., Ruiz,S., Savery,G.,
Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I.,
Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I.,
Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
Tansey,J., Taylor,C., Taylor,T., Telfrod,B., Thomas,N., Thomas,S.,
Ward-Moore,S., Warren,R., Washington,C., Watliamson,A., Wilczyk,R., Wooden,S., Warley,K.,
Wu,Y., Wu,Y., Wu,Y., Warren,R., Washington,C., Watlington,S.,
Wu,C., Wu,Y., Wu,Y., Shoo,J., Zorrilla,S., Nelson,D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (18-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 14, 2002 this sequence version replaced gi:20258282.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (11-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Worley, K.C.
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NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/eenbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently
consists of 59 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
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                                                                                                                                                                                                                                                                                                                                                                                                         Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 118901 bases at least Q40
Consensus quality: 125278 bases at least Q30
Consensus quality: 129335 bases at least Q20
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Center code: BCM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://www.hgsc.bcm.tmc.edu/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            College of Medicine
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accession

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AC113320
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E 2 (bases 1 to 188795)

E 2 (bases 1 to 188795)

E 3 (bases 1 to 188795)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barra, N., Bastlen, V., Boguslavkiy, L., Boukhgalter, B., Anderson, S., Barra, N., Bastlen, V., Boguslavkiy, L., Chazaro, B., Choepel, Y., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Cooke, P., Dearellano, K., Dewar, K., Diaz, J. S., Dodge, S., Faro, S., Cocke, P., Dearellano, K., Dewar, K., Diaz, J. S., Dodge, S., Faro, S., Ferreitra, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Plerre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Lancoque, K., Lamazares, R., Landers, T., Lehczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T.,
                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 188795)
Birren,B., Nusbaum,C. and Lander,E. Mus. musculis, clone RP23-445E16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21;
                                                                                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
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HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
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                                                                                                                                                                                                                                                                                                                                                                                         house mouse
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33755

unknown of 1379 unknown of 2093 unknown of 1533 unknown of 1241 unknown of 1485

bp in

Length

unknown

bp in

Length

3365

gap of contig gap of contig gap of contig gap of contig gap of contig

bp in

length

bp in

length length

28588

gap of contig

length

gap of contig gap of contig

bp in l

of 1647 unknown of 1150 unknown of 2014

length length

gap of contig gap of contig

unknown of 1321

bp in 1 length bp in 1

length

gap of contig gap of contig

f unknown
y of 1207
f unknown
y of 1143
f unknown
g of 1864

bp in l

Length length length length

gap of contig gap of contig gap of contig gap of contig

unknown of 1394 unknown of 1934 unknown of 1056 unknown of 1304

gap of contig gap of contig

40412: 40512: 42065: 42165:

f unknown y of 1553 f unknown y of 2258

37377: 38782: 38882:

of 2043 unknown of 1405 unknown of 1530

gap of contig gap of

bp in

length length

57683: 59735: 59835: 62023: 62123: 65327:

unknown of 2188 unknown of 2052

length bp in l length length bp in length bp in 1

unknown of 3204

contig gap of contig

of 2379 E unknown of 2080 I unknown of 2488

length bp in length bp in

unknown of 1759 unknown of 1401

> length length length

unknown

unknown of 2453

bp in

JOURNAL REFERENCE

AUTHORS

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Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S., Dodge, S., Farreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nayen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Feterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Divert, S., Sayer, A., and Zody, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 24, 2002 this sequence version replaced gi:18997726. All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkly,L., Boukhgalter,B., Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                           by the finished sequence the accession number will be preserved.

1 47353: contig of 47353 bp in length

47354 47453: gap of 100 bp

47454 48767: contig of 1314 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTE: This is a 'working draft' sequence. It currently
                                                                                                                                                                                                                                                                                                                       consists of 11 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequencing vector: Plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 185500 bases at least Q40 Consensus quality: 18954 bases at least Q30 Consensus quality; 187365 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center project name: L22784 Center clone name: 445_E_16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality coverage: 9.1 in Q20 bases; agarose-fp Quality coverage: 9.1 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center code: WIBR
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Insert size: 187795; sum-of-contigs
                                                                                                                                                                                                                                                                                the finished sequence as soon as it is available and
         48768 48867: gap of
48868 50642: con
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ρ of 100 bp contig of 1775 bp in length
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COMMENT

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Db 36223 AAGAAAAAATCTAGACAAACAA 36244
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                                                                                                                                                                                                                                                                                                                                                                                                                BASE COUNT
 REFERENCE
                                                                  SOURCE
                                                                                                                      ACCESSION
                                                                                                                                                    DEFINITION
                                                                                                                                                                                        AC069223/c
                                                                                  KEYWORDS
                                                                                                     VERSION
                                                                                                                                                                        COCUS
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                                                   ORGANISM
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                                                                                                                                                                                                                                                                                            1 AAGAAAAAATCTAGACAAGCAA 22
                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                         179767 bp
Homo sapiens 3 BAC RP11-398021 (
BAC Library) complete services
ACO60277
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1.79767)
                                                                                                     AC069223.15 GI:13489121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60813 60912:
60913 6276
62766 62865:
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52086 5457
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50743 519
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96248 188795: contig of 92548 bp in length
                                                                                                                                                                                                                                                                                                                              Conservative
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72530 72629:
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                                                                                                                                                                                                                                                                                                                                                                                                                               vector_side:right"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vector_side:left"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone_end:SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone_end:T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="assembly_fragment"
48868. .50642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-"assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="assembly_fragment"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="assembly_fragment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="assembly_fragment"
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                                                                                                                                                                                                                                                                                                                              92.7%; Score 20.4; 1
95.5%; Pred. No. 61;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            528: gap of 100 bp
58116: contig of 3488 bp in length
216: gap of 100 bp
60812: contig of 2596 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4/2: gap of 100 bp
5/12/3 bp in length
85: gap of 100 bp
85: gap of 24.43 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12: gap of 100 bp
62765: contig of 1853 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .188795
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           p of 100 bp
contig of 23518 bp in length
                                                                                                                                                      p DNA linear PRI 30-MAR-2001 (Roswell Park Cancer Institute Human
                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 188795;
                                                                                                                                                                                                                                                                                                                                                                                                                  1011 others
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                                                                                                                                                                                    Benton, J., Blankenburg, K., Bannin, D., Bouck, J., Banke, T., Bankenburg, K., Bonnin, D., Bouck, J., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burchl, K.L., Byrd, N.C., Carron, T.F., Chen, R., C
Direct Submission
                                                Worley, K.C.
                                                                                                           Unpublished
2 (bases 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MUZDY, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J.,
                                                                                       (bases 1 to 179767)
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REFERENCE JOURNAL AUTHORS AUTHORS Worley, K.C. Submitted (22-MAY-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 179767)

Submitted (30-MAR-2001) Human Genome Sequencing Center, Depar of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA On Mar 30, 2001 this sequence version replaced gi:13430920. INFORMATION: http://www.hgsc.bcm.tmc.edu/or email Department

COMMENT

JOURNAL

Direct Submission

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

## ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons

flanked by consensus splice sites that maintained continuity across the splice junctions. Sequences identical matches are annotated as similar Sequences that are not

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found quality are listed below. Description of the metrics can be found at URD: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation

## QUALSTAT-REPORT-----

bases	:	Position 3 107934 107935 159144	Contig length; Phrap values; Average error Fraction of P; Number of cone Number of N's
1000  900  900  700	Distribution of Quality < 40 Bases	n Original+Context  atccaaanaa(n)tctgatcttc atccgcggaa(t)tctgagactt gcctctttt(n)nacagagacta gcctctttt(t)acagagacta atggcaatca(n)cacacatggt atggcaatca(c)cacacatggt	Contig length: 179767 Phrap values in estimate: 179551 Average error rate (BCM-Phrap estimate): 4 4907e-06 Fraction of Phrap values less than 40: Number of consensus changing edits: 4 Number of N's in consensus: 0
		ottc gact acta	, , ,

	bases
	1000 900 800 700 600 500 400 300 100 100 0
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10	*
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15 20 25 Phrap Value Range	•
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35	* * * * * *
40	

Version:	Version: 1.01 gyfo
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source	1179767
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repeat_region	12021410
	/rpt_family="AluJb"
repeat_region	complement(40544428)
	/rpt_family="L2"
repeat_region	complement(4951, .5263)

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REFERENCE
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Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bomin,D., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C.,
                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                           BAC Library) complete sequence.
                                                                                                                                                                                                                                                                                                         Homo sapiens 3 BAC RP11-133K20 (Roswell Park Cancer Institute Human
                                                                                                                                                                                                                                                                                                                                 AC068763
                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                      AC068763.11 GI:14669935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                    (bases 1 to 180638)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /standard_name="G21620"
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(TFG), mRNA /cds=(18,1220) /gb=NM_006070 /gi=5174718
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(12041. .
/rpt_family="AluSp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /rpt_family="AluSq"
7302. .7547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Region similar to Homo sapiens mRNA; cDNA DKF2p586L2024 (from clone DKF2p586L2024); partial cds /cds=(0,1122) /gb=AL117664 /gi=5912260 /ug=Hs.58419 /len=2298"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="HAL1"
complement/1000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /rpt_family="MIR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(13142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /rpt_family="L1PA13"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88.2%;
95.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 19.4; DB 9; Length 179767; pred. No. 1.6e+02;
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AUTHORS JOURNAL

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Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,
Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O.,
Davy-Carroll,L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H.,
Dugan-Rocha,S., Dubbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C.,
Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J.,
Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T.,
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Ma,J., Mahsshwari,M., Mapua,P., Martin,R., Martindale,A.,
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Rojubokan,I., Rolfe,M., Riiz,S., Savery,G., Scherer,S.,
Sonaike,T., Sparks,A., Tamerisa,K., Tang,H., Tansey,J., Taylor,C.,
Taylor,T., Telfrod,B., Thomas,N., Thomas,S., Usmari,K., Vasquez,L.,
Vara,V., Villalon,D., Vinson,R., Wall,R., Wang,S., Ward-Moore,S.,
Milliamson,A., Milczyk,R., Wooden,S., Warren,K., Wu,Y.,
Milliamson,A., Tamerisa,K., Tang,H., Tansey,J., Taylor,C.,
Williamson,A., Martington,S., Land Gibbs,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (09-MAY-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                           Submitted (02-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, Tx 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (11-JUL-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Direct Submission
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                                                                                    Submitted (25-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 11, 2001 this sequence version replaced gi:13493008.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of Molecular and Human
Baylor Plaza, Houston,
4 (bases 1 to 180638)
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Direct Submission
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gc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                      Direct Submission
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                                          INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 180638)
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CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguittes or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

OWALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.

# QUALSTAT-REPORT-----

Number of N's in consensus :	Number of consensus changing edits:	reaction of Phrap values less than 40 :	Average error rate (BCM-Phrap estimate):	Phrap values in estimate:	Contig length:	Summary Statistics
0	49	0.00994637	1.00944e-05	179362	180638	

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tggctagg(n)gtggngcc	agetgettg(n)etage	tgacaatt(n)gctttt	aatacctat(n)ataattata	gcctccan(n)ccatttaa	tgcctcca(n)nccattt	aggganga(n)ggggtgg	gggaggga(n)gangggg	tttttt(g)gagagagtc	gctt(n)ttaacactc	cagctcct(n)gattcattg	(n)tgagtag	ttatta(n)tntgagtag	gccaccn(n)gcctggcct	agccacc(n)ngcct	ttgggat(n)acaggcgtg	ccatgcc(n)ggctaa	caaatan(n)tgg	ccaaata(n)ntg	)cctcccaa	n)tectgeet	n)c	cgcc(a)ccgcactcc	n)actccatct	agagct(t)nacto	caagagc(t)tnactccat	cttaaaaat(n)aaattttcg	aaataat(n)catgtacaa	t(n)gtatttct	cttcaggta(n)actgctca	ggctta(n)gatgtgtt	agaagan (n ) tggataaa	aaga(n)ntggat	atgagtgag(n)acgtgcgg	ttataga(n)aaaagagt	Original+Context	Consensus changing edits
cctggctagg(t)gtggtgcctc	Eccgggatt(t)tcctcc	tgataattc(t)gcttttt	:at(t)ataatt	ag(a)ccattta	ca(g)accattt	a(g)ggggt	ga (g) gaggggt	tt(t)qac	tt(t)tta	ccagctcct(q)qat	ttattatt(c)tqa	t) tot	t) acc	tgagccacc(q)	<u>.</u>	caccatocc(t)ooctaa	aataq(c)	tcccaaata(q)	cctqcctca(q)	caqqaqatt(c)	tcacctc(a)	gatcqcqcc(c)	caaqaqcqa(a)	acaaqaqcq(a)	acaagage(g)	aaaaat(t)	aaaataat(a)catqtaca	tcattatt(t)qtatttc	tcaqqta(a)actqctca	tggcttta(q)qatqtqtt	ctagaagaa(a)tggataaat	tctagaaga(a)atggataa	tgagtgag(a)acgtgcggt	tttataga(a)aaaagagtc	Edited+Context	ts

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Db 163480 AAGAAAAATCTAGACAGGCA 163500
                                                                                                               FEATURES
                                                                                   Query Match
                                                                      Best
                          1 AAGAAAAAATCTAGACAAGCA 21
                                                                   Local
                                                                                                                           Version: 1.01 qxfo.
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180511
180512
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151926
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                                                                                                                                                                                                                                                                                                           bases
                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                       Distribution of Quality < 40 Bases --
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aggtgngnnn(n)nnnntatggt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ctaggngtgg(n)gcctcacgcc
tagcacaatg(n)actttaagct
                                                                 88.2%; Score 19.4; 95.2%; Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gtgngnnnnn(n)nntatggtaa
                                                    0,
                                                                 Pred. No. 1.6e+02;
                                                                                                                                                                                             10
                                                   Mismatches
                                                                                                                                                                          Phrap Value Range
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                                                                               DB 9;
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gggatttcat(t)tatggtaact
ttgtaattca(a)aaaaaatttt
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aggtgggatt(t)catttatggt
ggtgggattt(c)atttatggta
ggtgggatttc(a)tttatggta
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                                                                             Length 180638;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        atactcagaa(t)aaaatccaaa
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                                                 Gaps
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RESULT 7 AC027080 REFERENCE SOURCE ORGANISM REFERENCE KEYWORDS ACCESSION VERSION DEFINITION AUTHORS TITLE AUTHORS JOURNAL Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Campoplano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., Firzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., 1 (bases 1 to 185841)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 3, clone RP11-548023 Unpublished Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Homo sapiens Homo sapiens. ACC27080 185841 bp DNA linear HTG 19-APR-21Homo sapiens chromosome 3 clone RP11-548023 map 3, WORKING DRAFT AC027080.2 GI:7596901 SEQUENCE, 22 unordered pieces (bases 1 to 185841) HTGS_PHASE1; HTGS_DRAFT. HTG 19-APR-2000

COMMENT

JOURNAL

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Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oilvar, T.M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Roy, A., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigillo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Nirsert, S., Zainoun, J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (26-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Apr 19, 2000 this sequence version replaced gi:7329443. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTE: This is a 'working draft' sequence. It currently consists of 22 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 172210 bases at least Q40 Consensus quality: 178990 bases at least Q30 Consensus quality: 181814 bases at least Q20 Theoret eight. 18070.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality coverage: 4.0 in Q20 bases; agarose-fp Quality coverage: 4.1 in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Whitehead Institute/ MIT Center for Genome Research
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Insert size: 183741; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8166 8265: gap of 100 bp 10 length 101612 11711: gap of 10 length 11612 11711: gap of 100 bp 11712 16128: contig of 4417 bp in length 16129 16228: gap of 100 bp 10228: gap of 100288: gap of 10
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61136
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50940 51039:
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                                                                                           51039: gap of 100 bp 10 length 61235: gap of 100 bp 10 length 61235: gap of 100 bp
                                                                                                                                                                                                                                                                                                      22213: gap of 100 bp 28574: contig of 6361 bp in length 28674: gap of 100 bp 34052: contig of 5378 bp in length 34152: gap of 100 bp 41388: contig of 7236 bp in length
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    69882: gap of
77230: con
                                                                      35: gap of 100 bp
69782: contig of 8547 bp in length
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                                                                                                                                                                                                                               gap of 100 bp
99: contig of 9451 bp in length
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contig of 2817 bp in length
contig of 7348
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            BASE COUNT
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121386 135542: contig of 14157 b
135543 135642: gap of 100 bp
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162025 185841: contig of 23817 bp in length
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147240 161924; contig of 14685 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="assembly_fragment" 61236 .69782
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/chromosome="3"
/map="3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="assembly_fragment" 98263. .109460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="assembly_fragment"
51040 61135
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22214. .28574
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        /note="assembly_fragment"
34837 c 33673 g 58130
                                                                                           /note="assembly_fragment"
162025. .185841
                                                                                                                                                                     /note="assembly_fragment"
147240. .161924
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/note="assembly_fragment"
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7239: config of 11497 t
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                        2110 others
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JOURNAL REFERENCE
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AC130437/c
         COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
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Best Local Similarity
                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
                                                                                                                                                                                                                                                             Rummolia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(CE 1 (bases 1 to 201416)

RS Muzny, D.M., Adams C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Buncy, D.M., Adems, C., Are, J.R., Ayele, M., Bryant, N.P., Buck, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Dabaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Dabhay, C., Burch, P., Burkett, C., Burcel, K.L., Byrd, N.C., Chen, G., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Dadhorne, S.R., David, R., Hart, R., Hart, M., Hale, S., Hanilton, K., Hart, M., David, R., Hale, S., Hanilton, K., Hart, M., Loud, R., Hale, S., Ha
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Submitted (10-AUG-2002) Human Genome Sequencing Center, Department of MoLecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                         Worley, K.C.
Direct Submission
                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                         Unpublished
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                                                                                                                                                                                           (bases 1 to 201416)
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95.2%;
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RESULT 9
AC022912
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                                    KEYWORDS
                                                         VERSION
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ORGANISM
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                                                                        unordered pieces.
AC022912
                                                                                                              AC022912 218859 bp DNA linear HTG Homo sapiens clone RP11-740L19, WORKING DRAFT SEQUENCE,
                                                         AC022912.3 GI:7596818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                               63751 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              be preserved.
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Consensus quality: 20030 bases at least Q40

Consensus quality: 216627 bases at least Q30

Consensus quality: 233347 bases at least Q20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         148169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Baylor College of Medicine Center code: BCM
              sapiens.
                                  HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                           Conservative
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/organism="Homo sapiens"
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/chromosome="3"
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95.2%;
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201416: contig of 53248
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99033: gap of unknown length
148068: contig of 49035 bp in
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                                                                                                                                                                                                                                                                                                                           Mismatches
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NCE, 34
                                                                                                                                                                                                                                                                                                                       0; Gaps
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ORIGIN

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (07-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Apr 19, 2000 this sequence version replaced gi:7158108.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J., McPheeters, R., McPan, J., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T. M., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Teefaye, S., Theodore, J., Martin, M., Subramanian, A., Talamas, J., Teefaye, S., Theodore, J., Martin, M., Subramanian, A., Talamas, J., Teefaye, S., Theodore, J., Martin, M., Subramanian, A., Talamas, J., Teefaye, S., Theodore, J., Martin, M., Martin, M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens, clone RP11-740L19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: This is a 'working draft' sequence. It currently consists of 34 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Assembly program: Phrap: version 0.960731 Consensus quality: 186472 bases at least (Consensus quality: 198582 bases at least (Consensus quality: 206779 bases quality: 206779 bases quality: 206779 ba
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Insert size: 185000; agarose-fp
Insert size: 215559; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center clone name: 740_L_19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center project name: L6286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://www-seq.wi.mit.edu
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9092: gap
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contig of 1051 lp
of 100 bp
                               100 bp contig of 1046 bp in length of 100 bp
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contig of 1186 bp in
of 100 bp
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120886 132423: contig of 11538 bp in
133424 132523: gap of 100 bp
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151891 170984: contig of 19094 bp in
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10213 11548: contig of 1336 bp in length
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           /note="assembly_fragment"
9093. .10112
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/clone_lib="RPCI-11 Human Male BAC"
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/db_xref="taxon:9606"
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35211: contig of 1796 bp in length
35311: gap of 100 bp
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...: gap of
14927: ~
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120785: contig of 11653
1885: gap of 100 b
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84412: contig of 10545 bp in length
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56549: contig of 6266 bp in length
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28906: contig of 3416 bp in length
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67: contig of 10107 bp in length
gap of 100 bp
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                2 (bases 1 to 274349) Waterston, R.H.
                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 274349)

Waterston, R. H.
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AC093623.1 GI:15487445
                                                 The sequence of Homo sapiens clone Unpublished
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96086. .109032
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84513. .95985
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53661. .73767
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14762. .50183
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29007. .33315
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22647. .25390
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|6467. .17996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              * NOTE: This is a 'working draft' sequence. It currently consists of 49 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chemistry: Dye-primer ET; 1% of reads chemistry: Dye-terminator Big Dye; 99% of reads chemistry: Dye-terminator Big Dye; 99% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 248392 bases at least Q40 Consensus quality: 257485 bases at least Q30 Consensus quality: 262193 bases at least Q30 Consensus quality: 262193 bases at least Q30
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Sequencing vector: plasmid; 998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site:http://genome.wustl.edu/gsc/index.shtml
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Submitted (07-SEP-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
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1489: gap of unknown length
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2656: gap of unknown length
3865: contig of 1209 bp in length
3965: gap of unknown length
5038: contig of 1073 bp in length
6762: contig of 1073 bp in length
6762: contig of 1624 bp in length
6862: gap of unknown length
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VERSION KEYWORDS

ACCESSION DEFINITION rocus AC093623/c RESULT 10

Matches Query Match

SOURCE

ORGANISM

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FEATURES
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                                                /note="assembly_name:Contig28"
6863. .8029
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/db_xref="taxon:9606"
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/note="assembly_name:Contig31"
                               /note="assembly_name:Contig30"
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                                                                                                                                                                                                                                    /clone="CTD-2335D13"
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J: gap of unknown length
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Oryza sativa (japonica cultivar-group)
Cryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                 APO05572 113940 bp DNA linear HTG 24-JUL-2002 Oryza sativa (japonica cultivar-group) chromosome 9 clone OJ1506_A04, *** SEQUENCING IN PROGRESS ***, in ordered pieces. APO05572
Published Only in Database (2002)
2 (bases 1 to 113940)
2 (bases 1 to 113940)
Sasaki,T., Matsumoto,T., Hattori,M., Sakaki,Y. and Katayose,Y.
Direct Submission
Submitted (23-UIL-2002) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan
                                                                                                                              Sasaki,T., Matsumoto,T., Hattori,M., oryza sativa nipponbare(GA3) genomic clone:OJ1506_A04
                                                                                                                                                                                                                                                                                          Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA
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/note="assembly_name:Contig32"

10542. 111788

/note="assembly_name:Contig34"

11889. .13219
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19157. .20355
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42171 . 45523
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39387. .42070
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23849. .25791
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="assembly_name:Contig39"
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95.2%;
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Pred. No. 1.5e+02;
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The nucleotide sequence of this BAC clone was generated by combining Monsanto and RGP-Japan sequencing data.

NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* NOTE: This is a 'working draft' sequence.

* this sequence will be replaced

* by the finished sequence as soon as it is available and cression number will be preserved.
                           of California, Berkeley, Rm. 265 LSA, Berkeley, CA 94720, Sequence updated by submitter On Oct 24, 2000 this sequence version replaced gi:1151128
                                                                                                                                                        Direct Submission
Submitted (07-DEC-1995) Molecular and Cellular Biology, Univerof California, Berkeley, Rm. 265 LSA, Berkeley, CA 94720, USA 4 (bases 1 to 2052)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygil; Neopterygil; Teleostel; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 2052)

Barth, A.L., Justice, N.J. and Ngai, J.
Asynchronous onset of odorant receptor expression in the developir zebrafish olfactory system
                                                                                            Submitted (08-JUL-1997) Molecular and Cellular Biology, University
                                                                                                                                                                                                                                                                                                                                   Noncoordinate expression of odorant receptor genes tightly linked in the zebrafish genome Neuron 19 (2), 359-369 (1997)
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Barth,A.L., Dugas,J.C. and Ngai,J.
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Location/Qualifiers
1. .2052
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/db_xref="taxon:39947"
/chromosome="9"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (28-MAY 1996) Data collected by MIPS on behalf of the European yeast chromosome XVI sequencing project. MIPS at the Max-Planck-Institut fuer Blochemie, Am Klopferspitz 18a D-82152 Martinsried, FRG; E-mail: Mewes@mips.embnet.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae

Eukaryota; Fungi, Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MIPS
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/translation="MLKIVTRAGHTARISNIAAHLLRTSPSLLTRTTTTTRELPFSTS SFLNHGHLKKPKPGEELKITFILKDGSQKTYEVCEGETILDIAQGHNLDMEGACGGSC
                                                                                                                         /note="ORF YPL252c"
                                                                                                                                    LNINWANLQKQNLERQVNHESQLRKDFTAFKEAKLKSMENLTNKHRELLDQIATLQSE SEKLHKEIMDIDRQAEYSEQNISEIN" complement(1264...1782)
                                                                                                                                                                                         /protein_id="CAA97977.1"
/db_xref="GI:2336844"
/db_xref="GI:2336844"
/db_xref="SPTREMBL:Q12045"
/db_xref="SPTREMBL:Q12045"
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RPSSMKSSLALPPYKDSFPSVSRSASLNINNSKIKDLKDRQDKIRFORHTLRTQLIEC
EREIKTIKFRDLNKSRFELYKKKSKQAKYLKQVRDLTQNLNSKDGERADLIKKNKSAL
ATLQAELDQNLILKRQDSQELYNNKLIFWENBLQIMENVEPDHEITEBISQLKKTLQE
                                         /protein_id="CAA97975.1"
/db_xref="GI:1370517"
/db_xref="SPTREMBL:Q12184"
                                                                                                     /codon_start=]
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/note="ORF YPL253c"
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/db_xref="taxon:4932"
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1 319 c 293 g 802 t
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/protein_id="AAC60253.1"
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/db_xref="taxon:7955"
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Pred. No. 6e+02;
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S.cerevisiae chromosome XVI reading frame ORF YPL253c.
Z73609 U00094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted (28-MAY-1996) Data collected by MIPS on behalf of the European yeast chromosome XVI sequencing project. MIPS at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a D-82152 Martinsried, FRG; E-mail: Mewes@mips.embnet.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
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3 362 c 474 g 773 t
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/note="ORF YPL251w"
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/note="ORF YPL253c"
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                                                                                                                                                                   DYENGVITQGLSEHVYKFNRVIPHLKVSEDKFFTQEYSVYHBMCLNQKKNFNLISLST
TPHGSLRESLIKFLAEXDTIYOKQYVITLOGENFOLDHLLDYSHNDKDSIKLK
FEKHSISLDSKLVIIENGLEDDLPHDSCDEHPNLPHSGMFJQDKIKVQFFPRDSKSDGNND
PVPVDFYFIELNNLKSIEQFDKSIFKKESCETPIALVLKKLISDTKSFFLLNLNDSKN
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    Score 18.8; DB 8; Pred. No. 5.9e+02;
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Saccharomyces cerevisiae
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LELVFSPSAASLEKSNTNHHSLYRLHNOLLLGIFAMSLERBNFLGRWGNESSWGFGNG
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                                                                                                                                                                                                       TPHGSLRESLIKFLAEKDTIYOKQYVITLQFVFLSDDEFSQDMLLDYSHNDKDSIKLK
FEKHSISLDSKLVIIENGLEDLPLNFSCDEHPNLPHSGMGIIKVQFFPRDSKSDGNND
                                                                                                                                                                                                                                                                                           NLKEMASKQEKFYNDTYNTVEKELLRSRRLENSIIEQKGTMRCYAYVMEQNLPENLLF
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SEKLHKEIMDIDROAEYSEONISEINENIKOLELANNPLISKSLONSODLEHLONOME
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                                                                                       /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78467, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GATC GmbH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLN 21-OCT-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                       DOWOILFNCILAIGAWCIEGESTDIDWYYONALELANDA
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SILVGRRIGLSONTISPESSVDDVGRTTTGFTIYHGIIETARLLOKPRIWGSVYSWEIGL
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TEKIQTCEKYIQVLEEVCAPFLLSQCAIFLLSNKSNAENNETAQLLQQINVVLMLIKKEL
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RSVTPFLGQQQQLQSLVPLTPSALFGGANFNOSGNIADSSLSFTFNSSNGPNIITTQ
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NTTMDDVYNYLFDDEDTPPNFKE"
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LDFMFRDALHGFDMSEEDDMSDGLPFLKTDPNNNGFFGDGSLLCILRSIGFKPENTY
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                                                                                                                                                                                                                                                                                                                                                                                                    complement(14010. .15581)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="GAL4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(11096. .13741)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DIKSQIEEEIRKQNLPNPDASLPKADLREDLERTISRNNEVNRENGQLEERITELQAE
IDELININKEQVSTASLLERDSKAKGRKGWTGFKKVFK"
                                                          translation="MDPFHNGNKRSSISFGSSQRQPYNKNNYLSGTNGPSSAAQDQGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="putative protein"
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complement(8054. 10738)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="SPTREMBL:Q12048"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MLKIVTRAGHTARISNIAAHLLRTSPSLLIRTTTTTTTTFLDFSTS
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ACSTCHVIVDPDYYDALPEPEDDENDMLDLAYGLTETSRLGCQIKMSKDIDGIRVALP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
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4025 AAGAAAAATCCAAACAAGCAA 4004

1 AAGAAAAATCTAGACAAGCAA 22

Matches Query Match

Local

Similarity

85.5%; 90.9%;

Score 18.8; DB 8; Length 37808;

3.8e+02;

Conservative

0

Mismatches

0; Gaps

0

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IEKLDSKKILPTDIQLKNLFPLKPKMLPIPSKPTLFDLAFNYITYDKQEPSASQVKDS
                                                ELPGYYSDDELLSQLDLCKLYFQLFLNTGCLSVLYQSKGRYMEALALYVDAYRRLENK
LSEIESLDEILLFANLLSLNSVRSLQKRIENGGNSVITLAEYEKRNHGGSLGKYDLTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /GL_XTEE="STTREMEL; Q12520"
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TLNLFVILWNILYFIVLDCKQMDNAVSVLTMDPQVWGYLMLYSFCGAMGQCFIFYTLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QFGSLVLIMITVTRKMVSMILSIIVFGKSVRFQQWVGMFIVFGGITWEALNKKKANIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="putative protein"
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/db_xref="GI:1061245"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(18399. .19418)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TLKDFYNEIPPKSRDWYTLKQQFRVAAPQNVLNWIDQISVAGKIPPIESVLSKGNADCADKIKNFDFKIWDDCGAMYEAIKEKDRQYGQCRMLSTYDFPYRLDGKDYYVECGDNFKVRWDRYTPREVTPWSERCDTIDEVGSYYTIQGFDLNYAGVILGRSIGYDAANDCIKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="SPTREMBL:Q12179"
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IVDEAHLLATSKDAFKRFYGENHLKDLMSLCKYLVLYYDDKQALRMGSYWDEGSNNGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="SRP68"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MNWKSYVEPGGHPPAALTTGLVVELTAIVLLSETFALREDLSLA
PESLEKLOMSRLSLYPLIHLSLPHLLENVLAIWAPLNLEEETHGTVYTGVFLNLSALF
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LVLLVAIAVVIPGSSFWGHFFGLCVGYAIGYXESWFNKITPPGWIITKIEKSLDGLIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GYAANIPVVSNLMNPSMASVCEYQSHYPLFGLDWSADDYVCLGSYKEDSRNKLOVLHS
NDLLSWESVVDADVVYPVSK.10WVPSQLYPRKLATCSDSLRIWSVSPEERQFQEQINL
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HGSSVMGIKWHPTKRNVLLSCGDDCQYLYWDLNSSFWEINAAGSKSPSIHGTSLEDPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16971. .18335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(15894. .16682)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GDTEMTDGGAGSGLNEDPLSLNNNSKQVCKTLETPNMMYANKTQEINNIAWRPQRGDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LIPWGIKYYRDEDIDRTKDYEPLMSTETPLPLHNDNSGTVLGTA"
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Search completed: March 17, 2003, 11:31:31 Job time : 548.495 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                          00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OM nucleic - nucleic search, using sw model
                 W41201200
                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
             17.8
17.4
17.4
17.4
17.2
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11:
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          80.9
79.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IDENTITY_NUC Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2185239 seqs, 1125999159 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l aagaaaaaatctagacaagcaa
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22
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SIDS2/gcgdata/geneseq/geneseqn-embl/NA198.DAT:*

SIDS2/gcgdata/geneseq/geneseqn-embl/NA199.DAT:*

SIDS2/gcgdata/geneseq/geneseqn-embl/NA1000.DAT:*

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SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
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                                                                                                                                                                                                                       DB
             ABQ69157
ABA12703
ABA18135
ABA18136
ABA18136
ABV37860
ABV58334
AAS30250
AAS30251
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Listeria monocytog
Human nervous syst
Human nervous syst
Human prostate exp
Human prostate exp
Human prostate exp
DNA encoding rena
DNA encoding rena
DNA encoding rena
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Atopy related	AAF 49331	4	0000			ć
Human	3 -	) i	1000	٠:	٦.	л.
Human	7 (	, c	24512	۳.	17.2	44
nullan		٥ ا	24512	٠:	7	43
	ABA19578	2	24512	ω.		42
Human	AAA34816	21	21742			41
Himar	AAF20938	21	21742	۳.		40
Homan	AA051024	14	11357	۳.		39
Human	AAF92144	22	11298			38
Human	AAA34815	21	11298			37
Human	AAF20937	21	11298			36
Human	AAV54661	19	11298			
Human	AAT86756	18	11298			4
Human	AAL36590	22	9615			(L
Human	AAK71750	22	7202	œ		2 2
Human	ABA19579	22	7202			) (A)
	ABL33783	24	6716	œ		3
pDIP/PyCSP.1	AAA58309	21	5552	œ		2 6
Human	AAK67062	22	4258	. 8		0 00
Human	AAF77689	22	4131			2 /
Drosophila	ABL16178	23	4081	. 8		26
Human wild	AAF77688	22	3729			25
Drosophila	ABL24782	23	3138			24
Drosophila	ABL22334	23	2963	8		23
Human cytokine rec	ABQ77508	24	2961	. 00		22
Drosophila melanog	ABL24452	23	2713	00		21
Human immune/haema	AAK83087	22	1622	8		20
Arabidopsis	508	21	1588	æ		1 4
Human	73	24	1509	78.2	17.2	18
Human	509	23	1372	8		1/
Oligonucleotide	371	24	831	œ		6
Oligonucleotide	371	24	831	0		. 5
Human colon speci	70	24	786	α		4
Extented	777	24	782	œ		٠ L
	AAS33486	22	674	æ		12
DNA encoding	3348	22	674	œ		-
Human	AAS26975	22	674	8		0

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#### ALIGNMENTS

RESULT 1
ABOG157
ID ABOG
XX ABOG
AC ABOG
XX ABOG
XX ABOG
XX ABOG
XX 29-A
XX Anti
XX Anti
XX Anti
XX Infe
COS List
XX WO2C
XX I1-A
XX WO2C
XX I1-A
XX (INS
PA (CNS
PA ( New genomic sequences from Listeria species, useful for detection, treatment and prevention of infection, also related polypeptides, WPI; 2002-332479/37. Kunst F, 04-OCT-2000; 2000FR-0012697. 04-OCT-2001; 2001WO-FR03061. (INSP ) INST PASTEUR.
(CNRS ) CNRS CENT NAT RECH SCI. 11-APR-2002 WO200228891-A2 Listeria monocytogenes 4b. Antibacterial; Listeria; food contamination; mutational analysis; infection; ds. Listeria monocytogenes 4b contig DNA sequence #1923 ABQ69157; ABQ69157 standard; DNA; 2483 29-AUG-2002 (first entry) Glaser P; ВP

AAS26974

2000US-0224519. 2000US-0225213.

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RESULT 2
ABA12703/c
ID ABA12703
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   RESULT
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04-FEB-2000
24-FEB-2000
02-MAR-2000
11-MAR-2000
11-MAR-2000
11-MAR-2000
19-MAR-2000
07-JUN-2000
28-JUN-2000
07-JUL-2000
07-JUL-2000
11-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to nucleic acid sequences (ABO67188-ABO71212) from Listeria sp. The sequences are useful as probes and primers for identification and/or detection of Listeria (e.g. as contaminants in foods, or mutational analysis) and for analysis of gene expression. Proteins encoded by the nucleic acid sequences can be used to screen for compounds that modulate gene expression, replication and pathogenicity of Listeria (potential therapeutic agents), also for treating infections by Listeria, and are useful as immunogens in
                                                                                                                                                                                                                                                                                                                      Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HTV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2483 BP; 771 A; 651 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   anti-Listeria vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antibodies and modulators
                                                                                                                                                                                                                          17-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                 Human nervous system related polynucleotide SEQ ID NO 1710.
                                                                                                                                                                                                                                                                                                                                                                                                                          23-JAN-2002 (first entry)
                                                                                                                                                                                                    31-JAN-2000;
                                                                                                                                                                                                                                               16-AUG-2001
                                                                                                                                                                                                                                                                     WO200159063-A2
                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                              neurological disease; infection; nephrotropic; gene therapy; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AAGAAAAAATCTAGACAAGCA 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAGAAAAATCCATACAAGCA 2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    printed specification, but was obtained in electronic fo
ly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard; cDNA; 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID 1970; 180pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
2000US-0184664

2000US-0189874

2000US-0199874

2000US-0190076

2000US-0199123

2000US-020515

2000US-0205467

2000US-0215135

2000US-0215135

2000US-0216647

2000US-0216647

2000US-0217496

2000US-0217496

2000US-0217496

2000US-0217496

2000US-021963

2000US-0217496

2000US-021963

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2000US-021963

2000US-021963

2000US-0220964

2000US-0220964
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2000US-0180628
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90.5%;
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Pred. No. 2.8e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 699 T; 0 other;
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     21-SEP-2000)
25-SEP-2000)
25-SEP-2000)
26-SEP-2000)
27-SEP-2000)
27-SEP-2000)
29-SEP-2000)
29-SEP-2000)
29-SEP-2000)
29-SEP-2000)
29-CCT-2000)
02-CCT-2000)
03-CCT-2000)
04-CCT-2000)
05-CCT-2000)
06-NOV-2000)
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08-NOV-2000]
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01-SEP-2000;
01-SEP-2000;
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22-AUG-2000;
22-AUG-2000;
22-AUG-2000;
22-AUG-2000;
23-AUG-2000;
30-AUG-2000;
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08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
12-SEP-2000;
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06-SEP-2000;
08-SEP-2000;
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14-AUG-2000;
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05-SEP-2000;
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2000US-0225268
2000US-0225477
2000US-0225477
2000US-0225758
2000US-0225758
2000US-02256681
2000US-0226681
2000US-0226681
2000US-022934
2000US-022934
2000US-022934
2000US-022934
2000US-022934
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2000US-023141
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2000US-0234998
2000US-0234998
2000US-0234998
2000US-0235834
2000US-0236369
2000US-02341808
2000US-0241188
2000US-0241188
2000US-02441826
2000US-02446474
2000US-02446475
2000US-02446475

0

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CC (ABB14678-ABB18001) useful for preventing, treating or ameliorating CC medical conditions e.g. by protein or gene therapy. The genes are CC isolated from a range of human tissues disclosed in the specification. CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital; CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative CC colitis; (c) cardovascular disorders such as myocardial ischaemias; C (d) wound healing; (e) neurological disease e.g. cerebral anoxia and C epilepsy; and (f) infectious diseases such as viral, bacterial, fungal c and parasitic infections.
            17-NOV-2000
01-DEC-2000
01-DEC-2000
05-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-NOV-2000

17-NOV-2000

17-NOV-2000
                                                                                                                                                                                                    useful for preventing, cancers and metastases
                                                                                                                                                                                                                      Nucleic acids encoding
                                                                                                                                                                              Claim 1; SEQ ID NO 1710; 1701pp + Sequence Listing; English
                                                                                                                                                                                                                                                       2001-541565/60.
                                                                                                                                                                                                                                            ABB16377
                                                                                                                                                                                                                                                                                                 HUMAN GENOME
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2000US-0246532.
2000US-0246609.
2000US-0246610.
2000US-0246611.
2000US-0246613.
2000US-0246613.
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2000US-0249209.
2000US-0249210.
2000US-0249211.
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2000US-0246526.
2000US-0246527.
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2000US-0249299.
2000US-0249300.
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2000US-0249216.
2000US-0249217.
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2000US-0249213.
2000US-0249214.
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2000US-0246524.
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2000US-0249265.
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2000US-0249245.
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2000US-0251856.
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2000US-0251988
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                                                                                                                                                                                                                                                                             SC,
                                                                                                                                                                                                                                                                                                  SCI INC
                                                                                                                                                                                                            3224 human
diagnosing
                                                                                                                                                                                                                                                                             Ruben
                                                                                                                                                                                                                                                                             SM;
                                                                                                                                                                                                            nervous system antigen polypeptides, and/or treating nervous system
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                                                                       14 - AUG
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RESULT 3
ABA18135/c
ID ABA18135 standard;
 14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
22-AUG-2000;
                                                                                                                                                                                                                                                         14-JUL-2000;
26-JUL-2000;
26-JUL-2000;
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30-JUN-2000;
07-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                          19-MAY-2000
07-JUN-2000
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24-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal;
antiparasitic; cardiant; immune disorder; cardiovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 370 BP; 130 A; 59 C; 60 G; 120 T; 1 other;
                                                                                                                                                                                                                      14-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-JAN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            neurological disease; infection; nephrotropic; gene therapy; vaccine;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nervous system related polynucleotide SEQ
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2000US-0225968
2000US-0224518
2000US-0224519
2000US-0224519
2000US-0225213
2000US-0225213
2000US-0225266
2000US-0225266
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2000US-02257575
2000US-02257575
2000US-0225758
2000US-0225758
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2000US-0217487.
2000US-0217496.
2000US-0218290.
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2000US-0198123.
2000US-0205515.
2000US-0209467.
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2000US-0216647
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94.78;
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Pred. No. 3
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2000US-0246474.
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2000US-0246478.
2000US-0246523.
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2000US-0246524.
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2000US-0236370.
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2000US-0235834.
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2000US-0227009
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2000US-0229509
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2000US-023399
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2000US-0233401
2000US-02334997
2000US-02344997
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                                               Q
                                                                                                                                                    Query Match
Best Local S
Matches 18
                                                                                                                                                                               The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune the haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (cd) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-NOV-2000
01-DEC-2000
                                                                                                                                                    Sequence 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 10466; 1701pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancers and metastases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-541565/60.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HUMA-) HUMAN GENOME SCI INC
                 220
                                   1 AAGAAAAAATCTAGACAAG 19
                 AAGAAAATATCTAGACAAG 202
                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Barash SC,
                                                                                  Conservative
                                                                                                                                                   BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0249208
2000US-0249210
2000US-0249211
2000US-0249211
2000US-0249213
2000US-0249213
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2000US-0249217
2000US-0249217
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2000US-0249264
2000US-0249297
2000US-0249297
2000US-0249299
2000US-0251160
2000US-0251160
2000US-0251166
2000US-02511866
2000US-0251866
2000US-0251868
2000US-0251868
2000US-0251868
2000US-0251868
2000US-0251999
                                                                                                                                                    137
                                                                                              79.1%;
94.7%;
                                                                                                                                                   A; 69 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3224 human nervous system antigen polypeptides, diagnosing and/or treating nervous system
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                                                                                  0,
                                                                                                  Score 17.4;
Pred. No. 3
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                                                                                                                                                   71 G; 135 T; 0 other;
                                                                                  Mismatches
                                                                                                  .8e+02
                                                                                                                   DB
                                                                                                              Length
                                                                                  Indels
                                                                                                                   412;
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22-AUG-2000)
22-AUG-2000)
23-AUG-2000)
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23-AUG-2000)
21-SEP-2000)
201-SEP-2000)
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209-SEP-2000)
209-SEP-

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ABA18136/C
ABA18136;
XX
Human nervous system related p
XX
Human, nootropic: neuroprotect
KW
Antiparkinsonian; antiinflamm
KW
Antiparkinsonian; antiistckilng
KW
An
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neurological disease; infection;
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    14 - SEP-2000
21 - SEP-2000
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25 - SEP-2000
27 - SEP-2000
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20 - CCT-2000
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08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
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14-SEP-2000;
2000US-0231244
2000US-0231244
2000US-0231281
2000US-0232881
2000US-0232397
2000US-0232397
2000US-0232399
2000US-02332401
2000US-02332401
2000US-0233064
2000US-0233063
2000US-0234231
2000US-0234231
2000US-0234231
2000US-0234231
2000US-0234283
2000US-0234884
2000US-0234884
2000US-0235834
2000US-0235834
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2000US-0249213
2000US-0249214
2000US-0249244
2000US-0249244
2000US-0249244
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ABV37860/C
ID ABV378
XX
AC ABV378
AC ABV378
DT 16-SEP
XX
DE Human
XX
KW Human;
KW Pharma
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17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
01-DEC-2000;
01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases -
                 Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       marrow, preast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification.
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 412
                                                                                                                                                                                                                                                                                                                                                                                                                                           Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format dir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and ovarian cancer and other cancers of the adrenal gland, bone, marrow, breast, gastrointestinal tract, liver, lung, or urogenita
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                                                                    Human prostate expression marker cDNA 37851.
                                                                                                       16-SEP-2002
                                                                                                                                          ABV37860;
                                                                                                                                                                        ABV37860 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breaming the diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 10467; 1701pp + Sequence Listing; English
                                                                                                                                                                                                                                                            220
                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                           1 AAGAAAAAATCTAGACAAG 19
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                                                                                                                                                                                                                                                            AAGAAAATATCTAGACAAG
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2000US-0256719.
2000US-0251479.
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2000US-0249297.
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2001US-0259678
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2000US-0251989.
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2000US-0251868.
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2000US-0251030.
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2000US-0249300
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                                                                                                     (first entry)
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94.7%;
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                                                                                                                                                                                                                                                                                                                                            Score 17.4;
Pred. No. 3
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                                                                                                                                                                                                                                                                                                                                              3.8e+02
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                                                                                                                                                                                                                                                                                                                                                            Length 412;
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RESULT 6
ABV58334/c
ID ABV583
XX ABV583
AC ABV583
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DT 13-SEP
XX
Human;
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(a) assessing whether a patient is afflicted with prostate cancer;

(b) monitoring the progression of prostate cancer in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in a patient;
(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) assessing the prostate cell carcinogenic potential of a compound;
(g) determining whether prostate cancer has metastasized in a patient;
(g) determining whether prostate cancer has metastasized in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 7745-7746; 11750pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-662795/76.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-JUN-2000;
18-JUL-2000;
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25-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Human prostate expression marker cDNA 58325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABV58334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABV58334 standard; cDNA; 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 434 BP; 130 A; 78 C; 76 G; 150 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  patient;(I) is also useful as a pharmacodyanamic or pharmacogenomic marker.
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                                                                                                                                                                                                                                                                                                           pharmacogenomic
                                                                                                                                                                                                                                                                                                                                               Human; prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-SEP-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (g) determining whether prosence cancer in assessing the aggressiveness or indolence of prostate cancer in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cancer in a patient;
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                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (d) assessing the efficacy of a therapy for inhibiting prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (c) assessing the efficacy of a test compound to inhibit prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240 AAGAAAAATCTTGAAAAGAAA 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AAGAAAAATCTAGACAAGCAA 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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2000US-207454P.
2000US-211314P.
2000US-219007P.
2000US-255281P.
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                                                                                                                                                                                                                                                                                                                marker;
                                                                                                                                                                                                                                                                                                                                                    cancer;
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86.4%; Pred. No. 4.6e+02;
                                                                                                                                                                                                                                                                                                                gene;
                                                                                                                                                                                                                                                                                                                                                    cytostatic; carcinogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Monahan JE
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RESULT 7
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Best Local :
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                                                                                                           Human; antiinflammatory; neuroprotective; immunomodulator; vulnerary; cardiovascular; cytostatic; nephrotropic; antianaemic; nephritis; immunosuppressive; kidney disorder; renal failure; hypertension; cardiovascular disorder; myocardial infarction; blood disorder; anaemia; blood coagulation disorder; electrolyte imbalance disorder; cancer; hyponatraemia; hypertalaemia; neoplastic disorder; nephtoma; autoimmune disease; inflammatory disease; reproductive system disorder; endocrine disorder; neural activity; neurological disorder; wound healing; respiratory disorder; ss.
             02-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer
                                                WO200155328-A2
                                                                                                                                                                                                                                                                                                       DNA encoding
                                                                                                                                                                                                                                                                                                                                          21-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                   AAS30250 standard; DNA; 674 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 507 BP; 179 A; 98 C; 93 G;
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18-JUL-2000;
13-DEC-2000;

(e) selecting a composition for inhibiting prostate cancer in a patier
(f) assessing the prostate cell carcingenic potential of a compound;
(g) determining whether prostate cancer has metastasized in a patient;
(h) assessing the aggressiveness or indolence of prostate cancer in a

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          296 AAGAAAAACACTAGTCAAGCAA 275
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25-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       is also useful as a pharmacodyanamic or pharmacogenomic marker.
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2000US-189862P.
2000US-207454P.
2000US-211314P.
2000US-2119107P.
2000US-255281P.
                                                                                                                                                                                                                                                                                                renal and cardiovascular-associated protein,
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86.4%;
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Pred. No. 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          134 T; 3 other;
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14-SEP-2000;
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2000US-0232399.
2000US-0232400.
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2000US-0231413
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2000US-0229513.
2000US-0230437.
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2000US-02148647
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2000US-0225768
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2000US-02256881
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2000US-0186350.
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17-NOV-2000;
                                                                               Rosen CA,
                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC.
                                                                               Barash SC,
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                                                                                      Ruben SM;
   RESULT 8
AAGS1021
IID AAGS3
XX AAGS3
XX AAGS3
XX DAG DNA
DT 21-N
DT 21-N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 В
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31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
18-APR-2000;
19-MAY-2000;
07-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; antiinflammatory; neuroprotective; immunomodulator; vulnerary; cardiovascular; cytostatic; nephrotropic; antianaemic; nephritis; immunosuppressive; kidney disorder; renal failure; hypertension; cardiovascular disorder; myocardial infarction; blood disorder; anaemia; blood coagulation disorder; electrolyte imbalance disorder; cancer; hyponatraemia; hyperkalaemia; neoplastic disorder; nephtoma; autoimmune disease; inflammatory disease; reproductive system disorder; neural activity; neurological disorder; wound healing; respiratory disorder; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAS30251;
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2000US-0184664.
2000US-0186350.
2000US-0189874.
2000US-0190076.
2000US-0198123.
2000US-0205515.
2000US-0209467.
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2000US-0180628
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86.4%;
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Score 17.2; DB 22 Pred. No. 4.6e+02; Mismatches

DB 22; Ψ

Length 674; Indels

0;

Gaps

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Seq ID 169

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30-JUN-2000

30-JUN-2000

07-JUL-2000

11-JUL-2000

11-JUL-2000

14-JUL-2000

14-JUL-2000

14-AUG-2000

10-SEP-2000

22-AUG-2000

23-AUG-2000

23-AUG-2000

23-AUG-2000

24-AUG-2000

25-SEP-2000

01-SEP-2000

01-SE
      01-SEP-2000
01-SEP-2000
01-SEP-2000
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20-CCT-2000
00-NOV-2000
01-NOV-2000
08-NOV-2000
017-NOV-2000
017-NOV-
                                                                                                                                                                    New polynucleotides and polypeptides, useful for diagnosing, treating, preventing or prognosing e.g. kidney, cardiovascular, blood, electrolyte imbalance or neoplastic disorders, autoimmune diseases, cancers -
The invention relates to novel nucleic acids and polypeptides useful diagnosing, treating, preventing and/or prognosing disorders related these polypeptides. The polynucleotides are especially useful in the diagnosis, prognosis, prevention and/or treatment of diseases which include kidney disorders (e.g. renal failure or nephritis),
                                                                                                                               Claim
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2000US-0246610.
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RESULT 9
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ID AAS2
XX AAS2
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XX DT 07-N
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CYCO
KW Huma
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24 FEB 2000
02 MAR 2000
116 MAR 2000
11 MAR 2000
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19 MAY 2000
07 JUN 2000
28 JUN 2000
28 JUN 2000
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07 JUL 2000
07 JUL 2000
11 JUL 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; immunosuppressive; antiarthritic; ds; antirheumatic; cytostatic; cardiant; vasotropic; cerebroprotective; nootro neuroprotective; antibacterial; virucide; fungicide; opthal vulnerary; secreted protein; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cerebrovascular disorder; cerebral ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; infection; ocu corneal infection; wound healing; epithelial cell proliferative skin ageing; food additive; preservative; antiproliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vulnerary; secreted protein; rheumatoid arthritis;
hyperproliferative disorder; cardiovascular disorder;
cerebrovascular disorder; cerebral ischaemia; angioger
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  2000US-0179065.
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2000US-0188350.
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2000US-0215135.
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antiproliferative.
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opthalmalogical;
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The invention relates to isolated nucleic acid molecules and their ce encoded secreted proteins. The nucleic acids and proteins are used to comprevent, treat or ameliorate a medical condition in e.g. humans, mice, crabits, goats, horses, cats, dogs, chickens or sheep. They care also used in diagnosing a pathological condition or susceptibility con a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in condition assays e.g. radioimmunoassays or enzyme linked condition condition assays or enzyme linked condition condition assays (ELISA). Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, conjugate to the protein assays (ELISA). Disorders which are diagnosed or treated conditionascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, viruses and fungicand ocular disorders e.g. corneal infection, and many other conditionation and condition also decreased in the specification. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to
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01-DEC-2000;
05-DEC-2000;
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06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
                                                                                                                                                                                                                                                                                                                                Novel polypeptides and polynucleotides useful as diagnostic reagents to diagnose diseases or disorders associated with aberrant expression or activity of polypeptides, for treating blood clotting disorder, haemophilia -
                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-476222/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID No 310; 601pp; English.
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19-MAY-2000;
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2000US-0190076. 2000US-0198123. 2000US-0205515. 2000US-0209467. 2000US-0214866. 2000US-0215135. 2000US-0216647.

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2000US-0220964. 2000US-0224518. 2000US-0224519.

2000US-0179065. 2000US-0180628. 2000US-0184664. 2000US-0186350. 2000US-0189874.

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prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be u as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The present sequence is a genomic DNA encoding a partial novel secreted protein
                                                                                              Human; immunosuppressive; antiarthritic; ds; antirheumatic; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiac arrest; hyperprolar disorder; cerebral ischaemia; angiogenesis; nervous system disorder; cerebral ischaemia; angiogenesis; nervous system disorder; hizheimer's disease; infection; ocular disorder; corneal infection; wound healing; epithelial cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                     Human genomic DNA encoding partial novel secreted protein,
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                                                               skin ageing; food additive; preservative; antiproliferative
Homo sapiens.
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Barash SC, Ruben SM;

WPI; 2001-476222/51.

Novel polypeptides and polynucleotides useful as diagnostic reagents to diagnose diseases or disorders associated with aberrant expression or activity of polypeptides, for treating blood clotting disorder,

Disclosure; SEQ ID No 311; 601pp; English.

e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection, and many other disorders listed in the specification. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be use as a food additive or preservative to increase or decrease storage encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays (ELISA). Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. never the breast or liver. capabilities, fat content, lipid, protein, carbohydrate, vitamins minerals, cofactors and other nutritional components. The present sequence is a genomic DNA encoding a partial novel secreted proteins The invention relates to isolated nucleic acid molecules and their novel secreted protein be used of

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                                cc encoding human secreted proteins (II) (I) and (II) are used to prevent, cc treat or ameliorate a medical condition in e.g. humans, mice, rabbits, cc gaats, horses, cats, dogs, chickens or sheep. (I) and (II) may be used in the prevention, treatment and diagnosis of diseases associated with C inappropriate expression of secreted proteins. (I) and complementary cs sequences may also be used as DNA probes in diagnostic assays (e.g. cof similar nucleic acid sequences in samples, and so which patients may complementary complementa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID No 768; 753pp; English.
                      cerebrovascular disorders (e.g. cardiac arrest,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention relates to novel isolated nucleic acid molecules (I)
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86.4%;
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Pred. No. 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.6e+02
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                      tachycardia,
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RESULT 12
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encoding human secreted proteins (II). (I) and (II) are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. (I) and (II) may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate expression of secreted proteins. (I) and complementary sequences may also be used as DNA probes in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect and quantitate the presence of similar nucleic acid sequences in samples, and so which patients may be in need of restorative therapy. (II) may also be used as antigens in the production of antibodies and in assays to identify modulators (agonists and antagonists may also be used to antipolate and antagonists may also be used to a proteins. The anti-(II) antibodies and antagonists may also be used to
                                                                                                                                                                                                                                                                                                                                                    New nucleic acids and polypeptides, useful for diagnosing, preventing or treating medical conditions - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rheumatoid arthritis; antiarteriosclerotic; cardiant; vascular; cerebroprotective; thrombolytic; antimicrobial; ophthalmological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fungi and ocular disorders (e.g. corneal infections). (I) and (II), agonists, antagonists and antibodies can also be used to promote wound healing, maintain organs before transplantation, and support cell culture of primary tissues. AAS33043-AAS33486 represent human secreted protein coding sequences. ACS3043-AAS33486 represent human secreted protein coding sequences, PCR primers, and related sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                    The invention relates to novel isolated nucleic acid molecules (I)
                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID No 769; 753pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-JAN-2001; 2001WO-US01347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaucher's disease; neurological disease; cerebrovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cytostatic; Alzheimer's disease; Parkinson's disease; humultiple sclerosis; cancer; hyperproliferative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunomodulatory; human immunodeficiency virus; HIV; anaemia; angina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding human secreted protein, Seq ID No 769.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   thrombosis; wound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  137 AAGAAAAAATTTAAACAAACAA
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86.4%;
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        may also be used as diagnostic agents for detecting the presence of (II) in samples (e.g. by enzyme linked immunosorbant assay (ELISA)). The disorders include for example: immunof-cultoimmune diseases (e.g. HIV (human immunodeficiency virus) infections, anaemia, rheumatoid arthritis and multiple sclerosis), cancers and hyperproliferative disorders (e.g. melanomas, neoplasms of the breast or liver, Sezary syndrome and Gaucher's disease), neurological diseases (e.g. Alzheimer's disease, parkinson's disease and Charcot-Marie-Tooth disease), cardio-/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Inflammatory bowel disease; IBD; autoimmune disorder; arthritis; allergy; haematopoietic cell; thrombolytic; blood coagulation disorder; nephritis; asthma; organ rejection; graft-versus-nost disease; inflammation; shock; nerve disease; Alzheimer's disease; Parkinson's disease; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   775/c
AAD37775 standard;
                                                                                        Claim
                                                                                                                           cells
                                                                                                                                            New polynucleotide associated with inflammatory bowel disease for treating disorders of the immune system, nervous system, hematopo
                                                                                                                                                                                                  WPI; 2002-426280/45.
                                                                                                                                                                                                                                                                      (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                       11-OCT-2000; 2000US-239712P
                                                                                                                                                                                                                                                                                                                                          11-OCT-2001; 2001WO-US32176
                                                                                                                                                                                                                                                                                                                                                                                                                 WO200231116-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Huntington's disease; immunosuppressive; sepsis; nephrotropic; nootropic;
neuroprotective; anticonvulsant; gene therapy; mouse; ds.
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                                                                                                                                                                                                                                     Sims
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                                                                                                                           modulate inflammation
                                                                                                                                                                                                                                     JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for mouse IMX5_09.
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86.4%;
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The invention relates to an isolated polynucleotide associated with inflammatory bowel disease (IBD). The invention is useful for manufacturing a medicament for use in preventing, treating, modulat

nufacturing a medicament for use in preventing, treating, modulating ameliorating a medical condition which is IBD. The polypeptide and

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ABQ73702/c ABQ73702 standard; cDNA; 786
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polynucleotide are useful for treating disorders of the immune system e.g. autoimmune disorders, deficiencies or disorders of haematopoletic cells, to modulate haemostatic, or thrombolytic activity, treat blood coagulation disorders, allergic reactions and conditions, such as asthma, treat and/or prevent organ rejection or graft-versus-host disease and modulate inflammation, including inflammation associated with infection,
cancer in a patient, by determining an amount of CSP or CSNA in a sample of a patient, and comparing it to the amount of colon specific marker in a normal control, where a difference in the amount of the nucleic acid or the polypeptide in the sample compared to that of normal control is associated with presence of colon cancer. CSP and CSNA sequences can be used for producing engineered colon tissue for treatment and research
                                                                                                                  polypeptide (CSP) sequences from the present invention. CSNA and CSP sequences have cytostatic activity, and can be used in gene therapy, antisense therapy and in vaccines. CSNA and CSP sequences can be used for diagnosing and monitoring the presence and metastases of colon
                                                                                                                                                                                                ABQ73695 to ABQ73841 represent human colon specific nucleic acid (CSNA) sequences, and ABP51826 to ABP51928 represent human colon specific
                                                                                                                                                                                                                                                                                                Colon specific polypeptides and polynucleotides useful for detecting, diagnosing, monitoring, treating, staging and predicting cancers in humans having cancer and non-cancerous colon disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; colon specific nucleic acid; colon specific polypeptide; CSP; CSNA; colon specific gene; CSG; colon cancer; gene therapy; vaccine;
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                                                                                                                                                                                                                                                             Claim 1; Page 153; 243pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (DIAD-) DIADEXUS INC
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86.4%;
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No. 4.7e+02;
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CC This invention describes a novel method for determining the degree of CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a GC genomic sample of DNA. The sample is treated chemically to convert CC cytosine (C) but not methylated C, to uracil, then part of the genomic CC The amplicon is hybridised to two classes, each with at least one CC member, of Oligonuclectides and/or peptide-nucleic acid (PNA) Oligoners CC and the degree of hybridisation to both classes is determined from the CC label on the amplicon. From the ratio of labels hybridised to the two classes of oligoners, the degree of methylation is calculated. The method CC is used: (1) for diagnosis and/or prognosis of side effects of the central nervous, cardiovascular, gastrointestinal and respiratory CC systems etc., particularly by detecting mutations or single nucleotide types and for investigating cell differentiation. The method allows the CC AB013410-AB054121 represent genomic DNA sequences used to illustrate the CC the disclosure of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABQ43712/c
ID ABQ43712 standard; DNA; 831 BP.
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Best Local :
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                                                                                                                                                                                                                                                                                                                                            Claim 12; 56pp + Sequence Listing; 56pp; German.
                                                                                                                                                                                                                                                                                                                                                                          Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA -
                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-371829/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-SEP-2000; 2000DE-1043826.
05-SEP-2000; 2000DE-1044543.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oligonucleotide for detecting cytosine methylation SEQ ID NO 30303.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 786 BP; 256 A; 118 C; 140 G; 272 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABQ43712;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Berlin K, Guetig D;
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Search completed: March 17, 2003, 10:50:47 Job time: 128.253 secs
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                                                       771 AAAAAAAATCTAAACAACCAA 750
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Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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## ALIGNMENTS

FEATURES source		COMMENT	TITLE	AUTHORS	REFERENCE	ORGANISM	KEYWORDS	VERSION	ACCESSION	DEFINITION	RESULT 1 AW740409
<pre>Email: nkr@helix.nih.gov, snailsrule@aol.com.     Location/Qualifiers     1. 342     /organism="Biomphalaria glabrata"     /strain="BS-90"     /db_xref="taxon:6526"</pre>	Blomedical Research Institute 12111 Parklawn Dr., Rockville, MD 20852, USA Tel: 301-481-3300 ext.128 Fax: 301-770-4756	Unpublished (2000) Contact: Raghavan N	Genes expressed by the hemocytes of Biomphalaria glabrata before and after exposure to miracidia	Raghavan,N., Miller,A., Gardner,M., Kerlavage,A.R., FitzGerald,P.C., Lewis,F.A. and Knight,M.	Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora; Planorbidae; Biomphalaria.  1 (bases 1 to 342)	Biomphalaria glabrata	EST.	AW740409:1 GI:7651688	Biomphalaria glabrata cDNA clone RBGIH55TR, mRNA sequence.	AW740409 342 bp mRNA linear EST 27-APR-2000 BRI10552 Biomphalaria glabrata (BS-90)-unexposed Lambda 7an tabrata	

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BASE COUNT
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BRI10646 Biomphalaria glabrata (BS-90)-unexposed Lambda Zap Library
Biomphalaria glabrata cDNA clone RBGIJ88TR, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genes expressed by the hemocytes of Biomphalaria glabrata before and after exposure to miracidia Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biomedical Research Institute
12111 Parklawn Dr., Rockville, MD 20852, USA
Tel: 301-881-3300 ext.128
Fax: 301-770-4756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Raghavan N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Raghavan,N., Miller,A., Gardner,M., Kerlavage,A.R., FitzGerald,P.C.,
Lewis,F.A. and Knight,M.
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Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nkr@helix.nih.gov, snailsrule@aol.com.
Location/Qualifiers
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                                                                                                                                                                                                         /Sea- networks // Sea- networks // Sea- networks // Sea- networks // Cell type="Hemocyte" // Cell type="Hemocyte" // Site_2: // Note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Total RNA was isolated from the hemocytes of sunexposed Biomphalaria glabrata (BS-90) snails and first strand cDNA synthesized using an oligo-dT primer-linker (XhoI). Second strand synthesis was followed by the ligation of EcoRI adaptors. Following digestion with XhoI, the completed, directional cDNA was cloned into Uni-ZAP
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68 c 62 g 80 t
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/clone_lib="Biomphalaria glabrata (BS-90)-unexposed Lambda
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/clone="RBGIJ88TR"
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/strain="BS-90"
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95.5%;
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Pred. No. 1.1e+03
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                                                                                                                                               vector by Stratgene.
63 g 78 t
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SOURCE VERSION

KEYWORDS ACCESSION

REFERENCE

COMMENT

JOURNAL TITLE AUTHORS

FEATURES

RESULT 2 BG360474

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RESULT 3
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BRI10553 Biomphalaria glabrata (BS-90)-unexposed Lambda Zap Library
Biomphalaria glabrata cDNA clone RBGIH56TR, mRNA sequence.
AW740410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora
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Biomedical Research Institute
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                                                                                                                                              BB016617 RIKEN full-length enriched, adult male testis (DH10B) Mus musculus cDNA clone 4930563D02 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: nkr@helix.nih.gov, snailsrule@aol.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 301-881-3300 ext.128 Fax: 301-770-4756
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                                     house mouse.
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/strain="BS-90"
/db_xref="taxon:6526"
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/lab_host="Laboratory host"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998) Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki
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Thermostabilization and thermoactivation of thermolabile enzymes by
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999) Carninoi, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
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                                                                                                                                                                                                                                        /lab_host-"pH108"
//lab_host-"pH108"
//note-"Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                               cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5'
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/db_xref="taxon:10090"
/clone="4930563D02"
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/dev_stage="adult"
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Length 224;
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             ,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
                                                                                 Zhao, S., Nierman, W., Feldblyum, T., Malek, J.,
                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 449)
                                                                                                                                                                                                                                                                                            RPCI-23-365C18.TV RPCI-23 Mus musculus genomic clone RPCI-23-365C18
                                                                                                                                                                                                                                       AZ009207.1 GI:7084591
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Class: sheared ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9712 Medical Center Drive, Rockville, MD 20850, USA. Tel: 301-838-3523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 424)
Town, C.D., Van Aken, S., Utterback, T. and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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                                                                                                                                                                                                                                                                                 DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="BO_2_3_KB"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
a 86 c 66 g 107 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BOMLK25"
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Pred. No. 3.8e+03;
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                                                  Shatsman,S., Akinret
K., Krol,M., de Jong,P.
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                                                                                                                        Murinae; Mus.
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 301 838 0200 Fax: 301 838 0208
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Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BB768795 RIKEN full-length enriched, B16 F10Y cells Mus musculus clone G370089D24 3', mRNA sequence.
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                                                                                                                                                          Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Szuuki,H., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Wattahiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 476)
Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T.,
Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K.,
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN)
                                                                                  Unpublished (2001)
Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note=*Organ: Kidney/Brain; Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-365C18"
/clone_lib="RPCI-23"
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BASE COUNT
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URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Y. and Hayashizaki,Y
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                                                                                                                                                                                                           Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST433300 KV1 Medicago truncatula cDNA clone pKV1-18B14, mRNA
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Unpublished (1999)
                           \mathtt{ESTs} from roots of Medicago truncatula 24 hours after inoculation with Sinorhizobium meliloti ^{\prime}
                                                                                                                                 VandenBosch, K., Endre, G., Hur, J., Moore, J., Beremand, P., Ellis, L.,
                                                                                                                                                                                                                                                                                                                                                                          BF004802.1 GI:10705077
                                                                               Fraser, C.M.
                                                                                                     Town, C.D., Bowman, C.L., Craven, M.B., Hansen, T.S., Holt, I.E. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="G370089D24"
/clone_lib="RIKEN full-length enriched, B16 F10Y cells"
/cell_type="B16 F10Y cells"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
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Pred. No. 3.8e+03;
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RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     528 bp mRNA linear Ezw93g12.rl Soares_total_fetus_Nb2HF8_9w Homo sapiens IMAGE:784582 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Department of Plant Biology
University of Minnesota
220 BioSci Center, 1445 Gortner Ave, St. Paul, MN 55108, USA
Tel: 612 624 2755
Fax: 612 625 1738
                                                                                     Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 475.
                                                                                                                                                                                                                                                                                                                           Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. Washr-Merck EST Project 1997
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Texas A&M University name: T268612e TIGR sequence name: MTIBJ07TK More information is available at: http://chrysie.tamu.edu/medicago Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 528)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: VandenBosch K
                                                                                                                                                                                                             Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                      Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                     Contact: Wilson RK
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//note="Vector: pBluescript SK -; Site_1: EcoRI; Site_2: XhOI; cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XLOLR cells."

a 93 c 103 g 164 t 1 others
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/dev_stage="24 hours post-inoculation with Sinorhizobium
meliloti"
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/culityar="genotype A17"
/db_xref="taxon:3880"
/clone="pKV1-18B14"
/organism="Homo sapiens"
/db_xref="GDB:5982200"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="KV1"
                                                                  Location/Qualifiers
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90.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Shaying Zhao, William Nierman, Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 7
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AQ414714 544 bp
RPCI-11-171019.TJ RPCI-11 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (info@resgen.com). BAC end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Map Building
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AQ414714.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: SP6
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113 c 91 g 169 t
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/note="Vector: pBACe3.6; Site_:
/notes="Vector: pBACe3.6; Site_:
/notes="Lymphocytes"
/no
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/clone_lib="Soares_total_fetus_Nb2HF8_9w"
/dev_stage="8-9 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="GDB:7565634"
                                                                                                                                                                                        /sex="Male"
                                                                                                                                                                                                                                                                                /db_xref="taxon:9606"
/clone="RPCI-11-171019"
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Pred. No. 3.7e+03;
                                                                                            pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
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                                                                                AAGAAAAAAACTAGACAAACAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.or
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
plate: 39 row: A column: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RAT BAC End Sequences from Library CHORI-230 EcoRI segment Unpublished (1999) other_CSSs: CH230-39A11.TJ Contact: Shaying Zhao Department of Eukaryotic Genomics The Institute for Genomic Research
 AQ534621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., (
,A., Gebregeorgis,E., Overton,L., Russell,D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Norway rat.
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CH230-39All.TV CHORI-230 Segment 1 Rattus
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Rat BAC End
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                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                         BAC ends.
                                                                                                                                                                                                                              ρ
                                                                                                                                                                                                                         /cell_type="Brain"
/note="Vector: pTaRBAC2.1; Sit
CHORI-230 Rat (BN/SSNHSd/MCW)
Pieter de Jong"
106 c 125 g 200 t
                                                                                                                                                                                                                                                                                                                                                                        /organism="Rattus norvegicus"
/strain="BN/SsNHsd/MCW"
                                                                                                                                                                                                                                                                                                            /sex="Female"
                                                                                                                                                                                                                                                                                                                          /clone_lib="CHORI-230 Segment 1"
                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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90.9%;
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90.9%;
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Pred. No. 3.7e+03;
0; Mismatches 2
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Pred. No. 3.7e+03;
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567 bp
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DNA
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                                                                                                                                                                                                                                                        Site_1: EcoRI;
CW) BAC library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  de Jong (pdejong@mail.cho.org).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MD 20850, USA
                                                                                                                                                                        17;
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                                                                                                                                                                            549;
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GSS 18-MAY-1999
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              Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AQ534621
AQ534621.1
                                                                                                                                                                                                                                                                                 1M0348C14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0348C14 F, DNA sequence.
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plasmid inserts
                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                 Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from (pieter@dejong.med.buffalo.edu).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Other_GSSs: RPCI-11-353P23.TJ
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
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Zhao, S., Adams, M.D., Nierman, W.,
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301 838 0208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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99 c 111 g 165 t
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/clone="RPCI-11-353P23"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cell_type="Lyr
/note="Vector:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="RPCI-11"
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/db_xref="GDB:7635550"
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"Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Primates; Catarrhini; Hominidae;
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Pred. No. 3
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RESULT 14
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Other_GSSs: RPCI-11-353P21.TJ
                            Unpublished (1997)
                                                           Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
                                                                                                         Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter
                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 597)
                                                     Map Building
                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                             AQ534617.1 GI:4846307
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Insert Length: 10000 Std Erro
Plate: 0348 row: C column: 14
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University of Utah Genome Center
University of Utah
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Location/Qualifiers
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Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                        DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"/note="Vector: PW042nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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/sex-"Male"
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90.9%;
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AUTHORS
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Best Local Similarity
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                                                                                                                                                                                                         Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TF
                                                                                                                                                                                                                                                                                                                                                                               Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001)
Other_GSSs: BOHQN17TR
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                                                                                                                                                                                                                                                                                                  9712 Medical Center Drive, Rockville, MD 20850, USA. Tel: 301-838-3523
                                                                                                                                                                                         Class: sheared ends.
                                                                                                                                                                                                                                                                                                                                                               Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 710)
Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Shaying Zhao, William Nierman, Mark Adams Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
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Clones are derived from the human BAC library RPCI-11. For BAC
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                                                          /organism="Brassica oleracea"
/strain="TO1000DH3"
/db_xref="raxon:3712"
/clone="BOHQN17"
/clone_lib="BOHQ"
/clone_lib="BOHQ"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
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/Ceil_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
/RPCII1 Human Male BAC Library"
107 c 115 g 174 t
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/clone="RPCI-11-353P21"
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/db_xref="GDB:7635548"
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genomic DNA inserted into pHOS1 using BstXI linkers"

BASE COUNT 209 a 146 c 149 g 206 t

ORIGIN

Query Match 85.5%; Score 18.8; DB 17; Length 710;

Best Local Similarity 90.9%; Pred. No. 3.5e+03;

Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGAAAAATCTAGACAAGCAA 22

Qy 1 AAGAAAAATCTAGACAAGCAA 133

Db 154 AAGATAAAATCTAGATAAGCAA 133

Search completed: March 17, 2003, 13:09:20

Job time: 782.688 secs

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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM nucleic - nucleic search, using sw model Run on: March 17, 2003, 09:43:42; Search time 230.108 Seconds (without alignments) 3161.870 Million cell updates/sec

Title: Perfect score: Sequence: US-09-836-439-5 25 gctttctttgctgagagctcttcca

25

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg: gb_om: *
gb_ov: *
gb_pat: *
gb_pt: *
gb_pr: *
gb_pr: *
gb_sy: *
gb_sy: *
gb_sy: *
gb_un: *
gb gb_ba:* gb_htg:* gb_in:*

em_htgo_other:* em_htgo_hum: *
em_htgo_mus: *

em_htg_mus: *
em_htg_pln: *
em_htg_rod: *
em_htg_mam: *
em_htg_vrt: *

em_htg_hum:*
em_htg_inv:*
em_htg_other:*

Pred. No. is the number of results predicted by chance to have

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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## ALIGNMENTS

REFERENCE AUTHORS TITLE		ORGANISM	SOURCE	SEGMENT	KEYWORDS	VERSION	ACCESSION	DEFINITION	Locus	MUSOPS4	prent n 1
<pre>1 (bases 1 to 269) Baehr,W., Falk,J.D., Bugra,K., Triantafyllos,J.T. and McGinnis,J.F. Isolation and analysis of the mouse opsin gene</pre>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	Mus musculus	Mus musculus (strain C56BL/6J) eye DNA.	4 Of 5	opsin.	M36698.1 GI:200149	M36698 X69175	Mouse opsin gene, exon 4.	MUSOPS4 269 bp DNA linear ROD 08-MAY-1993		

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RESULT 2
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                                                                                                                                     Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 31 Row: n Column: 2
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24;
                                                                                                                                                                                                                                                            Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.
Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                  cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (06-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2610 bp mRNA linear ROD 07-AUG-2
Mus musculus, clone MGC:25387 IMAGE:4527040, mRNA, complete cds.
BC031766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           About 117 bp after segment 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
                                                                                                                         analysis,
                                                                                                                                                                                                                                                                                                                                                                   Center code: BCM-HGSC
                                                                                                                                                                                                                                                                                                                                                                                        Sequencing Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="eye"
order(M36697.1:170.
/gene="opsin"
                /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="MGC:25387 IMAGE:4527040"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /number=3
15. .254
/tissue_type="Eye, retina, mouse strain C57B1\6"
                                                                                                  Location/Qualifiers
                                                                                                                         GenomeScan gene prediction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
/strain="C56BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31 Center Drive, Room 11A03,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       238 (2), 253-256 (1988)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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BC013125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (27-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus, Similar to rhodopsin (retinitis pigmentosa 4, autosomal IMAGE:4500760, mRNA, complete cds. BC013125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24;
                                                                                                 This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not
                                                                                                                                                                                         Clone distribution: MGC clone distribution
                                                                                                                                                                                                                                                       Gunaratne, P.H., Garcia, A.M., Lu, X., Yoon, V.S., Kowis, C.R., Lawrence, S.,
                                                                                                                                                                                                                                                                                                                                         Sequencing Center
Center code: BCM-HGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                             Series: IRAK Plate: 28 Row: e Column: 21
                                                                                                                                                                 through the I.M.A.G.
                                                                                                                                                                                                                               Richards, S., Gibbs, R.A.
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                                                                                 identity to protein.
                                                                                                                                                                                                                                                                                                 Contact: amg@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                     Web site: http://www.hgsc.bcm.tmc.edu/cdna/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
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                                     Location/Qualifiers
1. .3249
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ATASKTETSQVAPA"
1 727 c 656 g 623 t
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/protein_id="AAH31766.1"
/db_xref="GI:21594395"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WIMALACAAPPLVGWSRYIPEGMQCSCGIDYYTLKPEVNNESFVIYMFVVHFTIPMIV
IFFCYGQLVFTVKEAAAQQQESATTQKAEKEVTRMVIIMVIFFLICWLPYASVAFYIF
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                   /organism="Mus musculus"
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/translation="MNGTEGPNFYVPFSNVTGVVRSPFEQPQYYLAEPWQFSMLAAYM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
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/lab_host="DH10B"
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Pred. No. 1
                                                                                                                                                                   Consortium/LLNL at:
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autosomal dominant), clone MGC:21585
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Martin, R.G.,
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                                                                                                                                                                 http://image.llnl.gov
                                                                                                                                                                                         information can be found
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                                                                                                                                                                                                                                                       Hale, S.M., Muzny, D.M.,
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1 (bases 1 to 9483)
al-Ubaidi,M.R., Pittler,S.J., Champagne,M.S., Triantafyllos,J.T.,
McGinnis,J.F. and Baehr,W.
Mouse opsin. Gene structure and molecular basis of multiple
transcripts
transcripts
J. Biol. Chem. 265 (33), 20563-20569 (1990)
                                                                                                                                                                                                                                                                                                                                          91056108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
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/tlssue_type="Eye, retina, mouse strain C57Bl\6"
/clone_lib="NIH_MGC_94"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                         /gene-"MOPS"
                                                join(1434. .1794,3283. .3451,4525. .4690,4808. .5047,
                                                                             /gene="MOPS"
                                                                                                                    /gene-"MOPS"
                                                                                                                                                           5019. .9483)
/gene="MOPS"
                                                                                                                                                                                   )oin(1338.
                                                                                                                                                                                                                 /t1ssue_type="liver"
/dev_stage="adult"
                                                                                                                                                                                                                                                         /map="chromosome 6"
                                                                                                                                                                                                                                                                      /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                  /organism-"Mus musculus"
/product="opsin"
                                                                                                        'product="opsin"
                                                                                                                                            oin(1338.
                                                                                                                                                                                                "CISBUE_lib="EMBL3"
              /codon_start=1
                                                                                                                                                                                                                                             lone-"lambda-MO1"
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Pred. No. 1.
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                                    Indirana sp. Indirana sp.
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          Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranoldea; Ranidae;
                                                                                 AF249155.1 GI:12247239
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Indirana
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                                                                                                                                                                                                                                                      Conservative
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9410. .9415
/gene="MOPS"
a 2510 c 2
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/gene="MOPS"
8205. .8210
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/db_xref="GI:200145"
/translation="MMGTEGENFYVPFSNVTGVGRSDFEQPQYYLAEDWQFSMLAAYM
/LTANSlation="MMGTEGENFYVPFSNVTGVGRSDFEQPQYYLAEDWQFSMLAAYM
FLIIVLGFPINFLTLYVTVQHKKLRTPLNYILLNLAVADLFMVFGGFTTTLYTSLHGY
FYLIVLGEFINFLTLYVTVQHKKLRTPLNYILLNLAVADLFMVFGGENHAIMGVVFT
WIMALACAAPPLVGWSRYIPEGMQCSCGIDYYTLKPEVNNESFVIYMFVVHFTIPMIV
IFFCYGQLVFTVKEAAAQQQESATTQKAEKETTRMVIIMVIFFLICHLPYASVAFYIF
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/gene="MOPS"
9092. .9097
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7565. .7570
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6862. .6877
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9303. .9309
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7022. .7027
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                                                                                                                                                                                                                       Submitted (22-AUG-2000) Fischer C., Centre National de Sequencage, Genoscope, 2 rue Gaston Cremieux, CP5706, F-91057 Evry Cedex,
                                                                                                                                                                                                                                                                                                                                                                                             Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RHOD gene; rhodopsin.
Tetraodon nigroviridis.
                                                                                                                                                                                                                FRANCE
                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                 Fischer,C.
                                                                                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                Tetraodon nigroviridis gene for rhodopsin
                                                                                                                                                                                                                                                                                                                                                       Fischer,C.
                                                                                                                                                                                                                                                                                                                                                                                    Tetraodontidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AJ293018.1 GI:9909983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tetraodon nigroviridis rhod gene for rhodopsin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (27-MAR-2000) Unit of Evolutionary Genetics, Molecular Biology and Medicine, rue Jeener and Brachet Gosselies B-6041, Belgium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 175)
Bossuyt, F. and Milinkovitch, M.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 175)
Bossuyt, F. and Milinkovitch, M.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Convergent Adaptive Radiations in Madagascan and Asian Ranid Frogs Reveal Co-variation between Larval and Adult Traits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                 (bases 1 to 1062)
                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 1062)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
/codon_start=1
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/protein_id="CAC04526.1"
/db_xref="GI:9909984"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /number=4
3 54 c
                                                                      /gene="rhod"
                                                                                                       /gene="rhod"
                                                                                                                                         /organism="Tetraodon nigroviridis
/db_xref="taxon:99883"
                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="AAG49798.1"
/db_xref="GI:12247240"
/translation="AEKEVTRMYVIMVVFFLICWVPYAYVAFYIFTHQGSEFGPIFMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=2
/product="rhodopsin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Indirana sp./db_xref="taxon:147866"
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Pred. No. 8
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Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D., Weinstock,G. and Gibbs,R.
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Direct Submission

Submitted (17-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 178639)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (10-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA on Jul 9, 2002 this sequence version replaced g1:17941914.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
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NOTE: This is a 'working draft' sequence. It currently consists of 67 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap: version 0.990329
Consensus quality: 128571 bases at least 040
Consensus quality: 133786 bases at least 030
Consensus quality: 137554 bases at least 020
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Bossuyt,F. and Milinkovitch,M.C.
Direct Submission
Bufo melanostictus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Bufonidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (27-MAR-2000) Unit of Evolutionary Genetics, Institute Molecular Biology and Medicine, rue Jeener and Brachet 12, Gosselies B-6041, Belgium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 169)
Bossuyt, F. and Millnkovitch, M.C.
Convergent Adaptive Radiations in Madagascan and Asian
Reveal Co-variation between Larval and Adult Traits
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Mantella madagascariensis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Metazoa; Chordata; Craniata; Ranoidea;
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Bossiyt,F. and Milinkovitch,M.C.
Convergent Adaptive Radiations in Madagascan and Asian Ranid Frogs
Reveal Co-variation between Larval and Adult Traits
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Bossuyt, F. and Milinkovitch, M.C
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                                                                                                                                                                                      Molecular Biology and Medicine,
Gosselies B-6041, Belgium
Location/Qualifiers
                                                                                                                                                                                                                               Submitted (27-MAR-2000) Unit of Evolutionary Genetics, Molecular Biology and Medicine, rue Jeener and Brachet
                                                                                                                                                                                                                                                                    Bossuyt, F. and Milinkovitch, M.C. Direct Submission
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/protein_id="AAG49772.1"
/db_xref="GI:12247188"
/translation="AEKEVTRMVIIMVVFFLICWVPYATVAFFIFTHQGSEXGPIXMTIPAFFAKSSSIVNP"
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/db_xref="taxon:30335"
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/codon_start=2
/product="rhodopsin"
/protein_id="AAG49776.1"
/db_xref="GI:12247196"
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/db_xref="taxon:111290"
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                                              AF249136 175 bp DNA linear VRT 17 Boophis xerophilus rhodopsin gene, exon 4 and partial cds. AF249136
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Direct Submission

Submitted (27-MAR-2000) Unit of Evolutionary Genetics, Molecular Biology and Medicine, rue Jeener and Brachet Gosselies B-6041, Belgium

Location/Qualifiers
                            AF249136.1 GI:12247201
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1 (bases 1 to 175)

1 (bases 1 to 175)

Bossuyt,F. and Milinkovitch,M.C.

Convergent Adaptive Radiations in Madagascan and Asian Ranid Frogs

Reveal Co-variation between Larval and Adult Traits
                                                                                                                                                                                                                                      Similarity
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Bossuyt,F. and Milinkovitch,M.C.
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Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rhacophoridae;
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Vpaffakssaiynp"
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/db_xref="taxon:129014"
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                                                                                                                                                                                                                                  Score 20.2;
Pred. No. 52;
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Pred. No. 52;
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                                                                                           Submitted (27-MAR-2000) Unit of Evolutionary Genetics, Institute of Molecular Biology and Medicine, rue Jeener and Brachet 12, Gosselies B-6041, Belgium
                                                                                                                                                  2 (bases 1 to 175)
Bossuyt,F. and Milinkovitch,M.C.
Direct Submission
                                                                                                                                                                                                           1 (bases 1 to 175)
Bossuyt, F. and Milinkovitch, M.C.
Convergent Adaptive Radiations in Madagascan and Asian Ranid Frogs
Reveal Co-variation between Larval and Adult Traits
                                                                                                                                                                                                                                                                                                        Boophis tephraeomystax.
Boophis tephraeomystax
Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata;
                                                                                                                                                                                                                                                                                             Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea;
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                                                                                                                                                                                                      Unpublished
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Boophis xerophilus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Matrachia; Anura; Neobatrachia; Ranoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (27-MAR-2000) Unit of Evolutionary Genetics, Institute of Molecular Biology and Medicine, rue Jeener and Brachet 12, Gosselies B-6041, Belgium
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Bossuyt,F. and Milinkovitch,M.C.
Direct Submission
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Bossuyt,F. and Milinkovitch,M.C.
Convergent Adaptive Radiations in Madagascan and Asian
Reveal Co-variation between Larval and Adult Traits
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Similarity 88.0%;
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<1. .>175
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                                                                                          Location/Qualifiers
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Rhacophoridae;
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Gosselies B-6041, Belgium
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 175)
Bossuyt, F. and Milinkovitch, M.C.
Direct Submission
Submitted (27-MAR-2000) Unit of Evolutionary Genetics, Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bossuyt,F. and Milinkovitch,M.C. Convergent Adaptive Radiations in Madagascan and Asian Ranid Frogs Reveal Co-variation between Larval and Adult Traits
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Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea;
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AF249138.1 GI:12247205
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VPAFFAKSSAIYNP"
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Job time : 256.108 secs
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Bossuyt,F. and Milinkovitch,M.C.

Direct Submission

Submitted (27-MAR-2000) Unit of Evolutionary Genetics, Institute of Submitted (27-MAR-2000) Unit of Evolutionary Genetics, Institute (27-MAR-2000) Unit of Evolutionary Genetics, Institute (27-MAR-2000) Unit of Evolutionary Genetics, Institute (27-MAR-2000) Un
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Gosselies B-6041, Belgium
Location/Qualifiers
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Convergent Adaptive Radiations in Madagascan and Asian Ranid Frogs
Reveal Co-variation between Larval and Adult Traits
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/protein_id="AAG49782.1"
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/db_xref="taxon:128998"
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Pred. No. 52;
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Ranidae;
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Title:
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25
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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RESULT 2
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28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
                                          Claim 1; SEQ ID No 13141; 103pp; English.
                                                                                                                 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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23-AUG-2000; 2000US-0649167.
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The invention

relates to isolated polynucleotide (I) and

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CC Note: The sequence data for this patent did not appear in the printed contribution. In the other contribution in the printed contribution.
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPANK; SAM; sterile alpha motif; PARP; insulin resistance; poly adenosine diphosphate-ribose polymerase; catalytic domain; ANK; ankyrin repeat; cytosol; insulin-responsive aminopeptidase; IRAP; GLUT4; adipocyte; insulin signalling pathway; hyperlipidaemia; glucose intolerance; atheromatous disease; atherosclerosis; obesity; cardiac insufficiency; coronary insufficiency; stroke; high blood pressure; non-insulin dependent diabetes; hypertension; high blood pressure; non-insulin dependent diabetes; hypertension;
                                                                                                        WO200077225-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus.
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                                                              21-DEC-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hyperuricemia; Syndrome X; muscular dystrophy; muscle atrophy; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse SPANK cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 906 BP; 243 A; 218 C; 269 G; 176 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GCTTTCTTTGCTGAGAGCTCTTC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTTTCTTTGCTGCGATGTCTTC 655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                 /product= "Murine SPANK"
/transl_except= (pos:1754,aa:Gly)
/note= "This codon has an apparent 2 nucleotide
deletion, which alters the reading frame"
/transl_except= (pos:2145,aa:DTQIGKLLIG)
/note= "The nucleotides encoding residues 614 to 623
are absent, which alters the reading frame"
/transl_except= (pos:2602..2605,aa:Met)
/note= "This codon has an apparent 2 nucleotide
insertion, which alters the reading frame"
                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers 308..3254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72.8%;
87.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 18.2; DB 23;
Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
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AAAS3682

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AAS:

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DT 17-1

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CO) an AKK domain composed of ankyrin repeats.

SPANK is a cytosolic protein which can poly(ADP-ribosyl)ate itself.

SPANK is a cytosolic protein which can poly(ADP-ribosyl)ate itself.

SPANK is a cytosolic protein which can poly(ADP-ribosyl)ate itself.

SPANK is a cytosolic protein which can poly(ADP-ribosyl)ate itself.

SPANK binds insulin-responsive aminopeptidase [IRAP] and modulates

translocation of GLUT4 in the perinuclear region of adipocytes. It
is an effector in the insulin signalling pathway in eukaryotic cells.

SPANK is useful for reducing body mass, reducing glucose

intolerance or insulin resistance, for preventing or treating

obesity-related diseases or disorders, such as obesity, cardiac

insufficiency, coronary insufficiency, stroke, hypertension,

atheromatous disease, atherosclerosis, high blood pressure, non-insulin

dependent diabetes, hyperlipidaemia, hyperuricemia and Syndrome x and is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New insulin signalling protein SPANK, useful for reducing body mass, glucose intolerance or insulin resistance and for preventing or treating obesity-related and muscle-related diseases
                                                                                                                                                                                                                                   chicken; sheep; immunosuppressive; antiarthritic; vasotropic; dog; antirheumatic; antiproliferative; cytostatic; cardiant; neuroprotective; cerebroprotective; nootropic; antibacterial; virucide; fungicide; cancer; ophthalmological; vulnerary; gene therapy; autoimmune disease; neoplasm; hyperproliferative disorder; breast; liver; cardiovascular disorder; ds; hyperproliferative disorder; breast; liver; cardiovascular disorder; ds;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              also useful for preventing or treating muscle-related diseases or disorders, such as muscular dystrophy, muscle atrophy and muscle fatigue. Antibodies immunospecific for SPANK are useful for detections of the control of the control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3; Fig 5A; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-091404/10
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                                                                                                                                cerebrovascular disorder; nervous system disorder; bacterial infection; fungal infection; viral infection; ocular disorder; endocrine disorder; gastrointestinal disorder; renal disorder; respiratory disorder; wound healing; skin aging; organ transplantation; tissue regeneration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein comprises 3 domains:
(a) a SAM (sterile alpha motif) domain;
(b) a PARP (poly adenosine diphosphate-ribose polymerase) catalytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents the mouse SPANK cDNA. The SPANK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; AAB47023.
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                                                                                                                                                                                                                                                                                                                                                                   Cardiovascular system antigen; human; mouse; rabbit; goat; horse; cat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-DEC-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAS36854 standard; DNA; 6912 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3254 BP; 871 A; 746 C;
     WO200155321-A2
                                                      Homo sapiens
                                                                                                             anti-infertility.
                                                                                                                                                                                                                                                                                                                                                                                                                             Human cardiovascular system antigen genomic DNA SEQ ID No 2354.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     presence of SPANK polypeptide in a biological sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTATTTTGCTGAGAACTCTTCCA 2952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTTCTTTGCTGAGAGCTCTTCCA 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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87.0%;
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Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      863 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      774 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..7e+02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 3254;
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          14-SEP-2000;
14-SEP-2000;
21-SEP-2000;
21-SEP-2000;
25-SEP-2000;
25-SEP-2000;
26-SEP-2000;
27-SEP-2000;
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08-SEP-2000;
08-SEP-2000;
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01-SEP-2000;
01-SEP-2000;
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01-SEP-2000;
05-SEP-2000;
05-SEP-2000;
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22-AUG-2000;
22-AUG-2000;
22-AUG-2000;
30-AUG-2000;
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28-JUN-2000;
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08-SEP-2000;
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26-JUL-2000;
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07-JUL-2000;
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17-MAR-2000;
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2000US-0225775.
2000US-0225758.
2000US-0225758.
2000US-0225681.
2000US-0225681.
2000US-0225681.
2000US-02258681.
2000US-02258681.
2000US-02258924.
2000US-0229343.
2000US-0229343.
2000US-0229343.
2000US-0229343.
2000US-0229343.
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2000US-023948.
2000US-023948.
2000US-0231244.
2000US-0231413.
2000US-0233081.
2000US-0233081.
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2000US-0225266.
2000US-0225267.
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2000US-0218290
2000US-0220963.
2000US-0220964.
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2000US-0224519.
2000US-0225213.
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2000US-0233063
2000US-0233065
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2000US-0234997
2000US-0234894
2000US-0235484
2000US-02358834
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2000US-0216880.
2000US-0217487.
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2000US-0214886.
2000US-0215135.
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2000US-0180628.
2000US-0184664.
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2000US-0205515.
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WPI; 2001-451930/48

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13-OCT 2000
20-OCT 2000
01-NOV 2000
08-NOV 2000
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017-NOV 2000
17-NOV 2000
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11-NOV-2000
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17-NOV-2000;
        Rosen CA,
                          (HUMA-) HUMAN GENOME SCI INC
        Barash SC,
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2000US-0249244.
2000US-0249245.
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2000US-0249215.
2000US-0249216.
2000US-0249217.
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2000US-0249265.
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2000US-0246532.
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2000US-0241809.
2000US-0241826.
2000US-0244617.
2000US-0246474.
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2000US-0241221.
2000US-0241785.
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2000US-0241787.
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2000US-0249209.
2000US-0249210.
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2000US-0250160
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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CC Sequences AAS35741-AAS36942 represent genomic DNA molecules, which encode CC the cardiovascular system antigen polypeptides of the invention. CC Cardiovascular system antigens and their associated polynucleotides are useful in the diagnosis, treatment and prevention of various types of CC chickens or sheep. A pathological condition can be determined by CC detecting the presence or absence of a mutation in a cardiovascular cystem antigen polynucleotide. The treatable disorders include autoimmune CC system antigen polynucleotide. The treatable disorders liciude autoimmune CC diseases such as rheumatoid arthritis, hyperproliferative disorders such as cardiovascular disorders such as recardiovascular disorders such as cardiovascular disorders such as neoplasms of the breast or liver, cardiovascular disorders such as cardiac arrest, cerebrovascular disorders such as cerebral ischaemia, nervous system disorders such as Alzheimer's disease, infections caused by bacteria, viruses and fungi, ocular disorders such as corneal contection, endocrine disorders such as premature labour and infertility, gastrointestinal disorders such as premature labour and infertility, cas glomerulonephritis and respiratory disorders such as asthma and construction, to regenerate tissues and in chemotaxis.

CC prevent skin aging due to sunburn, to maintain organs before transplantation, to regenerate tissues and in chemotaxis.

CC prevent skin aging due to sunburn, to maintain part of the printed specification, but was obtained in electronic format directly from WIPO cc at fig. wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                  23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster genomic polynucleotide SEQ ID NO 31450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New cardiovascular system related polynucleotides and polypeptides, useful for diagnosing, treating and/or preventing disorders of the cardiovascular system -
                                                                                         WPI; 2001-656860/75.
                                                                                                                                                                                                                              (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                      23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pharmaceutical; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABL26659;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABL26659 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID No 2354; 674pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  647 TTTCTTTGCTGATAGCGGTTCCA 669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 TTTCTTTGCTGAGAGCTCTTCCA 25
                                                                                                                                                             JС,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                          Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                  2000US-191637P
2000US-0614150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72.8%;
                                                                                                                                                             ፫
                                                                                                                                                             PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 18.2; DB 22;
Pred. No. 1.9e+02;
""smatches 3;
                                                                                                                                                          Myers EW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 6912;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell

interactions

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RESULT 6
AAH515
XX
XX AAH515
XX
AC AAH515
XX
DT 29-AUG
XX
Human;
KW Human;
KW dipeyth
KW zileut
XX
Hoosph
KW JAPYI
XX
AN
XX
Hoosph
KW Zileut
XX
Hoosph
KW JAPYI
XX
AN
XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               flavin-containing monooxygenase; FMO; gamma-glutamyltransferase 5; dipeptidase; DP; glucose 6-phosphate dehydrogenase; G6PDH; haplotype; phosphogluconate dehydrogenase; PGDH; drug metabolism; phenotype;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; biallelic marker; single nucleotide polymorphism; SNP; MGSTII; microsomal glutathione S-transferase II; malate decarboxylase enzyme; DME1; ME1; cytochrome P450; glutathione reductase; GSHR; GSHS; GGT5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAH51547 standard; DNA; 756
Sequences AAH51110-AAH51593 represent human DNA fragments which contain biallelic markers. The sequences are related to various human genes including microsomal glutathione S-transferase II (MGSTII), malate decarboxylase enzyme (DME1/ME1), cytochrome P450, glutathione reductase/synthase (GSHR/GSHS), flavin-containing monooxygenases (FMO),
                                                                                                                                                                                                                                                     Polynucleotides comprising sequences from malate decarboxylase enzyme-related biallelic markers used for genotyping -
                                                                                                                                                                                                                                                                                                                                                                                                                Blumenfeld M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-MAR-1999;
30-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  zileuton; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human MGSTII related DNA containing a biallelic polymorphism SEQ ID 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 702 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          capable of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 31450; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-638353/61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200058508-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           uridine diphosphate glucoronosyl transferase; UGT2; asthma; hepatoxicity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              475 TCTTTCCTGAGCGCTCTTCCA 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB57737-ABB72072)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 TCTTTGCTGAGAGCTCTTCCA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19;
                                                                                                                                                                                        Page 616; 673pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   detecting 1000 or more genes from Drosophila. The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000WO-IB00403
                                                                                                                                                                                                                                                                                                                                                                                                                Bougueleret L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0126269.
99US-0131961.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             152 A; 190 C; 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71.2%;
                                                                                                                                                                                           English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 17.8;
Pred. No. 2e
                                                                                                                                                                                                                                                                                                                                                                                                                Chumakov I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G; 202 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                Cohen-Akenine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ST
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RESULT 7
AAH51581/c
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Qy
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CC Sequences ANH51594 - ANH51598 represent the genomic sequence of the

CC MGSTII gene and four alternative MGSTII cDNA sequences. ANB62906-ANB62906

CC are MGSTII gene products. PCR priners ANH51599 and ANH51600 are used in

CC an example for the amplification of human genomic DNA fragments. The

CC invention includes a method of genotyping comprising determining the

CI inventity of a nucleotide at a DME- or MGSTII-related biallelic marker in

CC a biological sample. The method is used to determine the frequency in

CC population of an allele of a DME- or MGSTI-related biallelic marker and

CC population of an individual for inclusion in a clinical trial of a drug

CC treatment. The method is also used to detect association between allele

CC and phenotype, and to detect association between haplotype and phenotype.

CC The polynucleotides are used, in hybridization assays, sequencing assays

CC or allele specific amplification assays. The method can be used to

CC determine whether an individual suffers or is at risk of developing

CC assume or is at risk of developing hepatoxicity on treatment with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gamma-glutamyltransferase 5 (GGT5), dipeptidase (DP), glucose 6-phosphate dehydrogenase (G6PDH), phosphogluconate dehydrogenase (PGDH), and uridine diphosphate glucoronosyl transferases (UGT2). Each of these sequences contains a biallelic marker/polymorphism, which is represented in the sequence as a degenerate/undefined base. The genes to which the biallelic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; biallelic marker; single nucleotide polymorphism; SNP; MGSTII; microsomal glutathione S-transferase II; malate decarboxylase enzyme; pMEI; MEI; cytochrome P450; glutathione reductase; GSHR; GSHS; GGTS;
                                                                      WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                    flavin-containing monooxygenase; FMO; gamma-glutamyltransferase 5; dipeptidase; DP; glucose 6-phosphate dehydrogenase; G6PDH; haplotype; phosphogluconate dehydrogenase; PGDH; drug metabolism; phenotype;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human MGSTII related DNA containing a biallelic polymorphism SEQ ID 472.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAH51581 standard; DNA; 1000 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                            Blumenfeld M,
                                                                                                                                                                                      25-MAR-1999;
30-APR-1999;
                                                                                                                                                                                                                                              24-MAR-2000; 2000WO-IB00403
                                                                                                                                                                                                                                                                                      05-OCT-2000
                                                                                                                                                                                                                                                                                                                          WO200058508-A2
                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                    uridine diphosphate glucoronosyl transferase; UGT2; asthma; hepatoxicity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        614 TTTCTTTGCTCAGAGCTCTCC 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 TTTCTTTGCTGAGAGCTCTTC 23
                                                                      2000-638353/61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             756 BP; 224 A; 140 C; 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                          Bougueleret L,
                                                                                                                                                                                      99US-0126269.
99US-0131961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71.2%;
90.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 17.8;
                                                                                                              Chumakov I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G; 213 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DΒ
                                                                                                              Cohen-Akenine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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Polynucleotides comprising sequences from malate decarboxylase enzyme-related biallelic markers used for genotyping -

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RESULT 8
AAS30820/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CC bhallelic markers. The sequences are related to various human genes.

CC charlelic markers. The sequences are related to various human genes.

CC decarboxylase enzyme (DMEI/MEI), cytochrome P450, glutathione

CC decarboxylase enzyme (DMEI/MEI), cytochrome P450, glutathione

CC reductase/synthase (GSHR/GSHS), flavin-containing monoxygenases (FMO),

CC gamma-glutamyltransferase 5 (GGTS), dipeptidase (DP), glucose 6-phosphate

CC diphosphate glucoronosyl transferases (UGT2), Each of these sequences

CC contains a biallelic marker/polymorphism, which is represented in the

CC sequence as a degenerate/undefined base. The genes to which the biallelic

CC marker containing sequences are related are involved in drug metabolism.

CC sequences AAH51594 - AAH51598 represent the genomic sequence of the

CC MSTII gene and four alternative MGSTII CDMA sequences. AAB62905-AAB62905

CC are MCSTII gene products. PCR primers AAH5159 and AAH51600 are used in

Invention includes a method of genotyping comprising determining the

CC identity of a nuclectide at a DME- or MCSTII-related biallelic marker in

CC abiological sample. The method is used to determine the frequency in

CC to select an individual for inclusion in a clinical trial of a drug

treatment. The method is also used to determine the frequency in

CC to select an individual for inclusion in a clinical trial of a drug

treatment. The method is also used to detect association between allele

CC The polynucleotides are used, in hybridization assays, sequencing assays

CC asthma or is at risk of developing hepatoxicity on treatment with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
08-MAR-2000;
08-MAR-2000;
08-MAR-2000;
08-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                      Human; G protein-coupled receptor; nGPCR-x; ss; antiviral; analgesic; cytostatic; cardiant; antidiabetic; anoretic; hypotensive; hypertensi antiparkinsonian; nootropic; neuroprotective; antidepressant; viral infection; HIV-1; human immunodeficiency virus; HIV-2; pain; cancer; metabolic disease; cardiovascular disease; type 2 diabetes; hander the context of the context of the cancer; metabolic disease; cardiovascular disease; type 2 diabetes;
                                                                                                      08-MAR-2001; 2001WO-US07322.
                                                                                                                                                   13-SEP-2001.
                                                                                                                                                                                                WO200166750-A2
                                                                                                                                                                                                                                                                                         obesity; anorexia; hypotension; hypertension; myocardial infarction; atherosclerosis; Parkinson's disease; psychosis; neurological disorder; schizophrenia; migraine; major depression; anxiety; mental disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-DEC-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human cDNA encoding G protein-coupled receptor nGPCR-2428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAS30820 standard; cDNA; 1000 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1000 BP; 300 A; 200 C; 211 G; 288 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequences
biallelic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 13; Page 641; 673pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      851 TTTCTTTGCTCAGAGCTCTCC 831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 TTTCTTTGCTGAGAGCTCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                         depression; dyskinesia; Huntington's disease; Tourette's Syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAH51110-AAH51593 represent human DNA fragments which contain
2000US-0187581.
2000US-0187582.
2000US-0187714.
2000US-0187715.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1000;
                                                                                                                                                                                                                                                                                                                                                                                                                        hypertensive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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Homo sapiens.

125..1654

Location/Qualifiers

/product= "ReproSA-1 protein"

ss; human;

vitro

fertilisation

Reprosa-1; contraceptive; anti-sperm; fertility;

0

Human ReprosA-1 coding sequence 14-DEC-1998 (first entry)

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RESULT 9
AAV59153
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                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    conditions such as infections, such as viral infections caused by HIV-1 (human immunodeficiency virus) or HIV-2, pain, cancers, metabolic and cardiovascular diseases and disorders (e.g., type 2 diabetes, obesity, ancrexia, hypotension, hypertension, myocardial infarction, atherosclerosis), Parkinson's disease, and psychotic and neurological disorders, including schizophrenia, migraine, major depression, anxiety, mental disorder, manta depression, and dyskinesias, such as Huntington's disease or Tourette's Syndrome and many other diseases and syndromes listed in the specification. nGCCR-x polynucleotides and syndromes listed in the specification modulators, may also be used in diagnostic assays for such diseases or conditions. The present sequence encodes a G protein-coupled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-MAR-2000;
08-MAR-2000;
08-MAR-2000;
08-MAR-2000;
08-MAR-2000;
08-MAR-2000;
08-MAR-2000;
                                                                                                                                                                                                                             AAV59153 standard; cDNA; 2573
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1000 BP; 265 A; 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to novel isolated nucleic acid molecules encoding 6 protein-coupled receptors termed nGPCR-x. nGPCR-x polynucleotides, polypeptides, and modulators may be used in the treatment of diseases and polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated nucleic acid molecules encoding G protein-coupled receptors termed nGPCR-x, useful in the treatment and diagnosis of viral infections, cancers and mental disorders (e.g. Parkinson's disease and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; Page 221-222; 336pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  receptor of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            schizophrenia) -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAU19251.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-MAR-2000;
08-MAR-2000;
                                                                                                                                                                                                                                                                                                      791 TTTCTTTGCTCAGAGCTCTCC 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PHAA ) PHARMACIA & UPJOHN CO
                                                                                                                                                                                                                                                                                                                             3 TTTCTTTGCTGAGAGCTCTTC 23
                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                              19;
                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wood LS;
                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0187825.

2000US-0187828.

2000US-01877829.

2000US-0187839.

2000US-0187839.

2000US-0187874.

2000US-0187874.

2000US-0187874.

2000US-0187894.
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2000US-0187928
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90.5%;
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                                                                                                                                                                                                                                                                                                                                                                         Score 17.8;
Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                  299 G;
                                                                                                                                                                                                                                                                                                                                                                                                                 228 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                        2.1e+02
                                                                                                                                                                                                                                                                                                                                                                                    DB 22;
                                                                                                                                                                                                                                                                                                                                                                                     Length 1000;
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RESULT 10
ABL26658
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The ReproSA-1 polypeptide, it's fragments, or nucleic acid encoding them are used in contraceptive vaccines to generate an anti-sperm response. Antibodies can also be used as topical contraceptive (spermicide), also antisense sequences, ribozymes and triplex-forming molecules. Detection, by reaction with immobilised peptides, of anti-(I) antibodies (in serum, semen, saliva, cervical or vaginal mucosa) is used to diagnose immunological infertility and to monitor the effect of vaccination. nucleotide fragments are used to diagnose infertility-associated mutations in the gene encoding Repro-SA, and for Isolation of related sequences. Peptides and anti-idiotypic antibodies against the antibodies are used to inactivate the antibodies i.e. to increase fertility and may be added to sperm samples before in vitro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sperm-specific polypeptide ReproSA-1 and related nucleic acid transformed cells and antibodies, useful in contraceptive vaccines or compositions, and for diagnosis and treatment of infertility
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 16; Fig 1; 62pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-FEB-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2573 BP; 754 A; 532 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (REPR-) REPROGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fertilisation.
                                                                                                                                                            Drosophila melanogaster
                                                                                                                                                                                     pharmaceutical; gene;
                                                                                                                                                                                                     Drosophila;
                                                                                                                                                                                                                            Drosophila melanogaster genomic polynucleotide SEQ ID NO 31447.
                                                                                                                                                                                                                                                        26-MAR-2002
                                                                                                                                                                                                                                                                                                             ABL26658
           (PEKE ) PE CORP
                                    23-MAR-2000;
11-JUL-2000;
                                                                              23-MAR-2001;
                                                                                                       27-SEP-2001
                                                                                                                                  WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                             252 TGTCTTTGCTGAGAACTCTTC 272
                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
les 19; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1998-480771/41.
                                                                                                                                                                                                                                                                                                                                                                                           TTTCTTTGCTGAGAGCTCTTC
                                                                                                                                                                                                                                                                                                              standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neilson LI,
                                                                                                                                                                                                    developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                        (first entry)
                                      2000US-191637P.
2000US-0614150.
                                                                              2001WO-US09231.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98WO-US03513.
                                                                                                                                                                                                                                                                                                                                                                                                                                             71.2%;
                                                                                                                                                                                                                                                                                                              3153 BP
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                                                                                                                                                                                                                                                                                                                                                                                                        23
                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 17.8;
Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       586 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       701 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                              2.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yamamoto KK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG1676-ABL30511), expressed DNA sequences (ABL08737-ABB16175) and the encoded proteins (ABB5737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1746 TCTTTCCTGAGCGCTCTTCCA 1766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3153 BP; 864 A; 693 C; 665 G; 931 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 31447; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster genomic polynucleotide SEQ ID NO 31369.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genes from Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Venter JC,
 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                       23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
                                                                                                                                                                                                                                                                                                                                                              WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                     pharmaceutical; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABL26632;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABL26632 standard; DNA; 3870
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                                                                        Claim
                                                                                                                 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cel
                                                                                                                                                                WPI; 2001-656860/75
                                                                                                                                                                                             Venter JC,
                                                                                                                                                                                                                                                                                                   23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                         (PEKE ) PE CORP NY.
                                                                                                      interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 TCTTTGCTGAGAGCTCTTCCA 25
                                                                      1; SEQ ID NO 31369; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19;
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                                                                                                                                                                                              Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                   developmental biology; cell signalling;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    isolated nucleic acid detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 17.8;
Pred. No. 2
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                                                                                                                                                                                              Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                         insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention
                                                                                                                       and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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cell-cell interactions in higher eukaryotes

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RESULT 12
AAD31629
ID AAD31
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AC ACAD1
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                                                                                                                Matches
                                                                                                                                                                  Query Match
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  6994
                                                                                                                                                                                                                                                                                           The invention relates to a polypeptide having GT1209, GT1354 or GT0946 activity obtained from Arabidopsis. The invention may also be applied to the development of herbicide tolerant plants, plant tissues, plant seeds and plant cells. The polypeptide is useful as herbicide targets in screening assays to identify potential herbicides and inhibitors of GT1209, GT1354 or GT0946 scitvity. A compound having herbicidal activity is useful for suppressing the growth of a plant. The newly discovered GT1209, GT1354 or GT0946 genes are essential for seeding growth and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polypeptide having GT1209, GT1354 or GT0946 activity, obtained Arabidopsis, useful as herbicide targets in screening assays to identify the inhibitors or potential herbicides -
                                                                                                                                                                                                                 Sequence 8002 BP; 2119 A; 1489 C; 1502 G; 2892 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 72-74; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-AUG-2000; 2000US-222779P
                                                                                                                                                                                                                                                                            development. The present sequence is Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Levin JZ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SYGN ) SYNGENTA PARTICIPATIONS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-2001; 2001WO-EP08910.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GT1209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana GT1209 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAD31629;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL1040-ABL16175) and the encoded proteins (ABBD18737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200212273-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAD31629 standard; DNA; 8002 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3870 BP; 961 A; 917 C; 886 G; 1106 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             103 TCTTTCCTGAGCGCTCTTCCA 123
                                                                                                                                          Local
                                                  2 CTTTCTTTGCTGAGAGCTCTT 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ç,
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CTTTCTTTGCTGATTGCTCTT 7014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2002-241730/29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene; herbicide; plant tissue; cell; seedling growth; development;
                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wegrich Glover L,
                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                    71.2%;
90.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71.2%;
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                                                                                                                                    Score 17.8;
Pred. No. 3e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 17.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Budziszewski GJ;
                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                    3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.7e+02;
                                                                                                                                                               DB 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 23;
                                                                                                          <u>ب</u>
                                                                                                                                                                                                                                                                   thaliana
                                                                                                                                                                                                                                                                   seedling growth and thaliana GT1209 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                       Indels
                                                                                                                                                            Length 8002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3870;
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                                                                                                 Gaps
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RESULT 13
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ID AAC079
XX AAC079
XX AAC079
XX Human
XX Human;
KW Gene t
XX Gene t
XX Gene t
XX Homo s
XX Homo s
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XX Homo s
PN EP1033
XX O6-SEP
XX 16-FEB
XX 16-
                                                                                                                                                                                                                              RESULT 14
ABL69358
XAXFXAX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNAS encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                  Prostate cancer related gene sequence SEQ
                                                                          15-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                           ABL69358;
                                                                                                                                                                                                  ABL69358 standard; DNA; 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID 12024; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is one of a large number of 5' ESTs derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GEST ) GENSET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human secreted protein 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                152 GCCTTCTTTGCAGAGATTTCTTCC 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                     1 GCTTTCTTTGCTGAGAGCTCTTCC 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20;
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herapy; chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               223 BP; 77 A; 38 C; 53 G; 54 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             223
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                                                                                                                                                                                                  ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 17.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO: 12024.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 21;
                     ID NO:7695
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18-SEP-2000;
20-SEP-2000;
20-SEP-2000;
20-SEP-2000;
22-SEP-2000;
25-SEP-2000;
25-SEP-2000;
25-SEP-2000;
25-SEP-2000;
25-SEP-2000;
25-SEP-2000;
25-SEP-2000;
26-SEP-2000;
27-SEP-2000;
27-SEP-2000;
27-SEP-2000;
27-SEP-2000;
28-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
20-CCT-2000;
20-CC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JUN-2000;
05-JUN-2000;
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The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change i expression of at least one gene (I) of a signature gene set, where (I)
                                                                                                                                             Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-DEC-2001
                                                                                                       Claim 1;
                                                                                                                                           determining
                                                                                                                                                                                                                           WPI; 2002-188264/24.
                                                                                                                                                                                                                                                                                                                             (AVAL-) AVALON PHARM
                                                                                                     SEQ ID 7695; 44pp; English.
                                                                                                                                                                                                                                                                   Augustus M, Weaver Z;
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2000US-237606P.
2000US-237608P.
2000US-244867P.
2000US-245084P.
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2000US-237294P.
2000US-237295P.
2000US-237316P.
2000US-237425P.
2000US-237598P.
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2000US-236033P.
2000US-236034P.
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2000US-236028P.
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2000US-237172P.
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                                                                                                                                                                                                                                                                                         Ebner
                                                                                                                                           gene
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                                                                                                                                             gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of MI, and the data is sufficient to convey the chemical structure and/or properties of the agent. MI can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
                                                                                                                                                                                                                                                                                                                                          25-MAY-2000;
09-JUN-2000;
18-JUL-2000;
13-DEC-2000;
                          The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) useful for:

(a) assessing whether a patient is afflicted with prostate cancer;

(b) monitoring the progression of prostate cancer in a patient;

(c) assessing the efficacy of a test compound to inhibit prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   infiltrating lobular cancer, squamous cell carcin carcinoma, papillary carcinoma and Wilm's tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 342 BP; 36 A; 109 C; 92 G;
                                                                                                                                               Claim 1; Page 1792; 11750pp; English
                                                                                                                                                                          Novel isolated nucleic acid molecule associated with cancerous state prostate cells and correlating with presence of prostate cancer, usef for detecting presence of prostate cancer, stage of prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human prostate expression marker cDNA 11060
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                                                                                                                                                                                                                                                                             Schlegel R,
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16-MAR-2000;
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2000US-207454P.
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83.3%;
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the efficacy of a therapy for inhibiting prostate cancer

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CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodyanamic or pharmacogenomic marker.

SQ Sequence 384 BP; 139 A; 87 C; 73 G; 85 T; 0 other;

Query Match
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 CTTTCTTTGCTGACAGCTCTTCCA 25
Db 374 CTTTCTTTGCGGAAGCTATTTCA 351

Search completed: March 17, 2003, 10:50:50

Job time: 146.446 secs
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Gapop 10.0 , Gapext 1.0
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gb_est2:*
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Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

റ	Result
	esult No. Score
999999 88 99999	% Query Match
93.6 405 93.6 495 93.6 628 93.6 636 93.6 649 93.6 651	% Query Match Length DB
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12 BE950666 13 BT737699 13 BT734160 13 BT75487 12 BG403992 13 BT730233	ID
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38365 60336112	62056 60237389	14191 00335114	JANG AGENCOOL	SERVICE SCHOOLS	21973 ACENCOLE	93203 60239015	32985 AGENCOUR	37919 60335749	39561 60336181	39285 60335957	37918 6033574	93614 6023902	72123 6033964	29984 6033500	04226 6024202	32279 60335420	34568 6033564	36361 6033600	61526 6023732	72453 6033980	97332 6023954	93849 6023903	98242 6023963	373234 6033975	04627 6024207	5000	2002200 201000	734477 6033571	738044 6033571	137113 IIT-M-CE	735675 6033578	298167 6023963	737008 6033608	295809 6023932	735044 6033561	736996 6033608	298553 6023969	729678 6033493	730180 6033497

ALIGNMENTS

	COMMENT	JOURNAL MEDLINE	TITLE	AUTHORS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	RESULT 1 BE950666/c
National Institute of Mental Health 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD 20892-9643, USA Tel: 301 443 1706 Fax: 301 443 9890 Email: mEST@mail.nih.gov The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site	Contact: Chin, H	Genome Res. 6 (9), 791-806 (1996) 97044477	Normalization and subtraction: two approaches to facilitate gene discovery	Bonaldo, M.F., Lennon, G. and Soares, M.B.	1 (bases 1 to 402)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciuroonathi; Muridae; Murinae, Murinae	Mus musculus	house mouse.	EST.	BE950666.1 GI:10589332	BE950666	MAP_Ret3 Mus musculus	BE950666 402 bp mRNA linear EST 29-ADR-2002	

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RESULT 2
BI737699
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24;
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                                                                                                                                             cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: McC clone distribution: McC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 495)
                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Location/Qualifiers
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/lab_host="pH108 (Life Technologies)"
/lab_host="pH108 (Life Technologies)"
/note="vector: pT7T3D-Pac (Pharmacia) with a modified
/note="vector: pT7T3D-Pac (Pharmacia) with a modified
/note="vector: pT7T3D-Pac (Pharmacia) with a modified
/note="vector: pT7T3D-Pac (Pharmacia) with a library is derived from mouse retina tissue.
For a detailed description of the library from which this
clone was derived, please visit our web site at
brainest.eng.ulowa.edu. The tissue for this library was
contributed by Dr. Xin-Yuan Fu, Yale University School of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/strain="C57BL/60"
/db_xref="taxon:10090"
/clone="UI.M-CE0-aza-d-06-0-UI"
/clone_lib="NIH_BMAP_Ret3"
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a 86 c 126 g
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/db_xref="taxon:10090"
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Pred. No. 19
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NIH-MGC http://mgc.nci.nih.gov/.
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Tissue Procurement: The Cepko Laboratory
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Contact: Robert Strausberg, Ph.D.
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Plate: LLAM11912 row: h column: 09
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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/lab_host="pHIOB (phage-resistant)"
/lab_host="pHIOB (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
/note="SalI; Cloned unidirectionally; oligo-dT primed.
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

Note: this is a NIH_MGC Library."
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/clone_lib="NIH_MGC_94"
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/tissue_type="retina"
/tissue_type="retina"
/lab_host="DH10B (phage-resistant)"
/note="0rgan: eye; Vector: pCMV-SPORT6; Site_1: NotI;
/notice="0rgan: eye; Vector: pCMV-SPORT6; 
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Pred. No. 23;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 649)
                                                                                        NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Location/Qualifiers
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Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lnl.gov
Plate: LLAM11936 row: j column: 13
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Tissue Procurement: The Cepko Laboratory
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Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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                    Tissue Procurement: The Cepko Laboratory
                                    Email: cgapbs-remail.nih.gov
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cDNA Library Preparation: Life Technologies, Inc
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/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 651)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                             CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        603350201F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:5357472 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 644.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 539.
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Plate: LLAM11909 row: b column:
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            /clone_lib="NHH_MGC_94"
/tissue_type="retina"
/lab_host="DHIOB (phage-resistant)"
/note="organ: eye; Vector: pCMV-SPORT6; Site_1: Not1;
/site_2: Sali; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies Note: this is a NHH_MGC_Library."
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/lab_host="hH10B (phage-resistant)"
/lab_host="hH10B (phage-resistant)"
/note="Organ: eye: Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: eye: Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NHLMGC Library."
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/clone="IMAGE:5357472"
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                                                                                                                                                                                              GCTTTCTTTGCTAAGAGCTCTTCCA 426
                                                               mRNA sequence.
BI729678
                                                                                   BI729678 663 bp mRNA linear EST 20-8EF-2 603349362F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:5356959 5',
                                                                                                                                                                                                                                                              24;
Mus musculus
                house mouse
                                                BI729678.1 GI:15706691
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM11908 row: p column: 06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="retina"
/lab_host="DHIOB (phage-resistant)"
/not="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
                                                                                                                                                                                                                                                                                                                                       /clone="IMAGE:5357429"
/clone_lib="NIH_MGC_94"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/db_xref="taxon:10090"
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                                                                                                       DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM10395 row: i column: 10
                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko_Laboratory
                                                                                                                                                                                                                                                                                                                                                  NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria;
1 (bases 1 to 672)
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1 (bases 1 to 663)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
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http://image.llnl.gov
Plate: LLAM11907 row: 1 column: 16
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Clone distribution: MGC clone distribution information can be
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                                                                                   e: LLAM10395 row: i column: quality sequence stop: 666.
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//db_xref="taxon:10090"
//clone="IMAGE:5356959"
//clone_lib="NIH_MGC_94"
//tissue_type="retina"
//tissue_type="retina"
//tab_host="DH10B (phage-resistant)"
//note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
//note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
//site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
56 a 209 c 151 g 147 t
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/organism="Mus musculus"
/db_xref="taxon:10090"
                                                                 Location/Qualifiers
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96.0%;
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Rodentia;
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Pred. No. 24;
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GCTTTCTTTGCTAAGAGCTCTTCCA 433
                                      GCTTTCTTTGCTGAGAGCTCTTCCA 25
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus
1 (bases 1 to 676)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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BI736996
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603360842F1 NTH_MGC_94 Mus musculus cDNA clone IMAGE:5367875 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 662.
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                                                                                                         Similarity
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                                                                                    Conservative
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//lab_host="DHIOB (phage-resistant)"
//note="organ: eye; Vector: pCMV-SPORT6; Site_1: Not1;
/note="organ: eye; Vector: pCMV-SPORT6; Site_1: Not1;
/site_2: Sal1; Cloned unitdirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
44 a 214 c 160 g 158 t
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/clone_lib="NIH_MGC_94"
/tissue_type="retina"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: Not1;
/site_2: Sali; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

a 206 c 156 g 160 t
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Pred. No. 24;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 682)
11 (hases 1 to 682)
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18 (hases 1 to 682)
19 (hases 1 to 682)
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Tissue Procurement: The Cepko Laboratory
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BI735044
                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies,
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BG295809
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                                                                                            Contact: Robert Strausberg, Ph.D
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National Institutes of Health, Mammalian
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Plate: LLAM11924 row: h column:
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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/clone="lib="NH_MGC_94"
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/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/lab_nost="Organ: eye; Vector: pCMV-SPORT6; Site_1: Not1;
/note="organ: eye; Vector: pCMV-SPORT6; Site_1: Not1;
/site_2: Sal1; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NHLMGC Library."
52 a 220 c 156 g 152 t 1 others
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96.0%;
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Pred. No. 24
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BI737008 694 bp mRNA linear EST 20-SEP-2001 603360855F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:5368117 5',
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10378 row: g column: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 694.
Location/Qualifiers
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Plate: LLAM11936 row: m column:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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                                                                                                                                            /tissue_type="retina"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Syle="color: blue;">Average insert size 3.3 kb. Library enriched for the primed for 
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/db_xref="taxon:1090"
/clone="IMAGE:4505134"
/clone_lib="NIH_MGC_94"
/tissue_type="retina"
/lab_host="PH10B (phage-resistant)"
/lab_host="PH10B (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
                                                                      full-length clones and constructed by Life Technologies Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:5368117"
/clone_lib="NIH_MGC_94"
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603357821F1 NIH_MGC_94 Mus
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                                                                                   mRNA sequence
BI735675
                 Mus musculus
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Contact: Robert Strausberg, Ph.D
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Eukaryota;
                                 house mouse.
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/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
/site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 %b. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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/db_xref="taxon:10090"
/clone="IMAGE:4507824"
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/tissue_type="retina"
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Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                      Ouery Match 93.6%; Score 23.4; DB 13; Length 697; Best Local Similarity 96.0%; Pred. No. 24; Matches 24; Conservative 0; Mismatches 1; Indels 0.
                                                                     585 GCTTTCTTTGCTAAGAGCTCTTCCA 609
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RS NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
AL Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tisue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
High quality sequence stop: 697.
SS Location/Qualifiers
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22
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Pred. NO. Ė the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

Theileria parva Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileriidae; Theileria. complete cds. AF198437 L36964 AF198437.1 GI:11545211 AF198437 17938 bp DNA linear INV 05-DEC-2000 Theileria parva strain Muguga hypothetical telomeric SfiI fragment 20 protein 3, hypothetical telomeric SfiI fragment 20 protein 2, and hypothetical telomeric SfiI fragment 20 protein 1 genes, Theileria parva. (bases 17114 to 17938)

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE

RESULT 1 AF198437 LOCUS

DEFINITION

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (25-0CT-1999) Unit 5, International Livestock Research Institute (ILRI), Old Naivasha Road, Nairobi p.O. Box 30709, Ken On Dec 5, 2000 this sequence version replaced gi:624245.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polymorphic open reading frames encoding secretory proteins are located less than 3 kilobases from Theileria parva telomeres and. Biochem. Parasitol. 110 (2), 359-371 (2000)
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SSTSGNIHTFTSGVSHSAVDASQGASVLDSGSSSSTLVLTEYKRLPSIRLTTSTDTDT
SSKSQTATPVTTTTNVALDIDKKQSTDQFEYSDINNYRIYVAKTNFVFNKIVQGTTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="hypothetical telomeric SfiI fragment 20 protein _{3}^{\mathrm{m}}
                                                                                                                                                                                                                                                                                                                     STSYNTREKELTDDNSELSTSDYKVTVAEHCYNLEFNSDVKCSKITHNGADLWKHSD
DTOFGTIKSLHLILINNQLGLKNQSNTLKELQAPLPPTPDVTDTTGTKITIDLABTKE
VEGMETYSHDGKCHTVATAGFGNTFGKVMKGTRVVWEPVGNQAKKIIYVDDHVKNVV
VVLTDGKFLLLKQSDNNWDDVTKYTLDVSKLVFLGDNHGATSLGVSASVTVVDTAMTL
TPDDQSKLISGSASSSPVTSPVSQPKSATVTTTPATTPQTQGPAPAKVPEAKSTTTTA
PQVSGPAVTBSTATPSPAKVTSFPAATLSGTEVTPFKVAVSGFVTLDIDNTQSASEY
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VQGTDEVWKSQVLFGTKVTAAGDFLTILLNNGTFKLFQKSVGEWIDITPNKHDIGKLK
FYGEGDRLLKSYDYSVTLSCLAFSYEFNVGSECHKVKYGDDVLMHSDDSQFGTIKTF
SLDLFKNQFTIKNNSGTVKNVEFKYVILDLNTMESTDHFDRTGDDGIFKFVVKSGYVF
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SQPKATAATIGTSTPTTPPTPTTSAAQTKATPTTGARPATQPKVTPASASSTQPKSQA
NVTPVSGSAAPSVSTSATPTKPVSQSTPTTSVTKVTLNIDTTKESTSELDYSKIGDIH
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sttpksqnqtqssqsqsestasatsrrrtgttgaqgsqptkppsqpassngsgshasp
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GDRDTEIKSSKYSVTMSGLSYNLDFNTNVDCKKIKYNNVTLWSHTDDSEFGTIKSLSL
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/strain="Muguga"
                                                                                              CKKITLDNYTLWSHTDDTOFGTIKSFSLGLVLNGFFIKNESGTVKPAEPTKVTLDIEK
TQSTVQLEYKVQNGVVTYTGKDCHVFSKIMQGSTVVWESEENLFATKVIKDCNKNSLS
                                                                                                                                                                                               TLGNIIYNYQDDTDFGSIGSLDLDLVSNGFFVKNESGDLKSVTKPVILDLETTKSTP
EFDISYIEGSDHIYIPKENRVFNKVVRGPTLIWESKDNVCATIVTISSKFLSILFDNN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="AAG37800.1"
/db_xref="GI:11545212"
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                                                                                                                                                                 TFKLFQESEKQWTDITSDRHNVASLKFYGDNNVEIKLSDYIVSMSGLSYNFEFKTGVK
                                                                                                                                                                                                                                                                                          DYKDEGGVVTYTPKENHVFSKVTEGPIVLWKSDDVSGTMVRICSKLLVILFNNNEFKL
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                                                                      INLSNGTTKEFQQSDSKWTESQTSSPVTTSSSSAQTATTETATTGTTTTTKTVLDIDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .10840
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ATSATOPTOGTT PESVIGEPTEKS PESTITTON ONVSTITOS VPPT PIGTTVTS VTLDI
ATSYTDPTOGTT PESVIGEPTEKS PESSITTTON ONVSTITOS VPPT PIGTTVTS VTLDI
NTTNSTQOFECKEKNGVIS YVAKSGNVETKVUHGOTS VMESSANVSGAMVTTKKDEFI
AILLDINKKFLIFONSDNKMTDOSKTTTDDDTKTLDDTTSSOYK IVLSDLSY NLQ
PNDGVKCSKITHKGVRWPUPDOSKTTTDDDTKTLDDTTSSKSASDDTGFGFIKSL
HLDLVANKFSVKNESDQVKEFEYKPVKSKITTSSGGTLSVDAVPGLYKLNGLTOSO
VDIVKYOKSFEYHFK PNVKCSMILFNDDTTSYTHETVNNS PNDDVFGTKVVVSDDVK
YLLLLLNNMYKMFTHFY NNKWPLIS RORRDVSKLKFYGIQEVSDSSSSLTVPBSDRQL
TPSDYKFSISDFVFSFENNEGILCRKINGDMIVYNYDILKTPIKSFNINLRINQFSV
NNRFGDANVELVQRPDTLITIDLNVCETTFEXQYLKTDDDFHTYVPLGYAFNINGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISGLKFITDDSBIGTSDYKVTISCHSYILEFNPGVECHKITHRGIDLWKSDDDQKFK
SVKSLSLCLLSNQLSVTNESGTYKDLKLTSDTTETESTAPPTKYITLDVDKKQSTSEF
ECKEKNGVTSYTAKSDIVFTKITHKTTVVWESGGNVCALLVSVKAEFLALLLSNUÇKF
LFQKSSDGTWKDITSQRHNISNLKELGQGGSVLKSPDYSVSMSGLILVYEFNTKCTKI
MLENENIWKPDDDPKFFKIKSLSLDIANNKFSLKSDTAVKELELSLATSTESATKSAT
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kqgnvtrytkonavmddsknddyclkaiymdhnspkylavilosgkevliyraayd
viersdtnnnithoruvtkikflgdssaviloassyebtiadryysfefkngakckki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="hypothetical telomeric 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNDIWESTTDCSLKVVYMDSAKLLAILMDNNKFFLFQESSGTFRDITSMRHDVSNLKF
                                                                                                                                                                                                                                                                                                            LLPTPESTTVSPELTTLAPESTTVIPDQTETTATFAESTSSYNPSTLDLNTRNSTRDF
DYSKTDNVHVYTAKSNHSESKITRGSNTVWEAPDNVSAKSVIFVDESIKYVTIDLGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DDH1FTPKSGCEFSKVVRGEKVIWEASENLFAKDVIFDEANNYVT1ELTNGSFRTITL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LGLVSNKFFVKNQSDQLKMIEYRPGTLPIVTDVNRNTSSELDIDKKGSTDRYDYENNG
                                                                                                                                                                                                                              KQLLKLEQPLPLNQQMLLPHM"
                                                                                                                                                                                                                                                                         FYRTVQVDPKSQTNTKTNNTRTKNIPLILLVPLILLPPTLLTLLILLLKHLLLLKKQ
                                                                                                                                                                                                                                                                                                                                                                                               KFGDDVLWKHDSEFGQIVSFHLDLISNKFFLKNHNGDVKSIEYTTGSLKVTTVTTNCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /evidence=not_experimental
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/product="hypothetical telomeric Sfil fragment 20 protein
                                                                 /evidence=not_experimental
                                                                                                    /codon_start=1
                                                                                                                                               /note="ORF1"
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FTEKAGVNCKRINYGDVVIWTHTDDKFEYITNFDLDLVKNEFFVFDDKRKSRKVNYEG PIISSYTPRTASASTPSTPKYQYASATKVTLDISKTQFTCFEXSLKSGVIRTFTPRSN CFIIKVTHCTTVIWESKTDVFGIRVTYVDVVKYLFLLLDNDKFLLFHQPPDRNKPWID /translation="MIGHWLFINLLLYITLLCOMNSVVTYSISSTSAKQITLDINKTT STNDSDYSKNGKYRTFTAKPGKSFNKVVKKKLYIWECKNNDQAVKVVLMGSGNNKKHL LILLKSSNFVILYKTGRNKPWINITSKRHDPTNLKFFOIDKELTSSDYEVTIYEFSYR 17698. PPPPYSESQHDTPETPSYPPPPYSESQHDTPEPPSYPPPPYSESQHEAPQ SDDTDFGY1KSLL1DLVANKFRVKNDSGQLKKLDFKPSTPRL1F1FEQQYQQAPPQSR PTPTYPRPP1PARPPYPSHQLFVQPQP1HPGPQLSVRQPVRPPAYSE1QYDTPETPSY /protein_id="AAG37802.1" /db_xref="GI:11545214" ITYTRVNLSKLKFFAENDMELKSTDYSVNLVSYSYSLEFNAGVKCQKVKYGNEDVWTN

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/rpt_type=tand~~ /note="telomeric repeat" /function="stabilizes en /rpt_unit=17698. 3549 c 3098 .17715 5814 t of chromosome" Length 17938;

Query Match 88.2%; Score 19.4; DB 3; ORIGIN BASE COUNT

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SOURCE
ORGANISM
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AUTHORS
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JOURNAL
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On May 15, 2001 this sequence version replaced gi:13751581.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr6 RP1-11688 is from the library RPCI-1 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                    IMPORTANT: This sequence is not the entire insert of clone RP1-11688 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP11-13J16 is at 42109 in this sequence. The true right end of clone RP3-483L3 is at 100 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (12-MAY-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VECTOR: PCYPAC:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tromans, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 42208)
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                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
  3125. .3190 
/note="33 copies 2 mer ca 66% conserved"
                                                                                                               /note="MIR repeat: matches 156. .262 of consensus"
                                                                                                                                                                            /note="MLT1B repeat: matches 1. .383 of consensus"
                                                                                                                                                                                                                                                                    /clone="RP1-116B8"
                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                           clone_lib="RPCI-1"
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ne 6, complete
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                                                                                                                  /note="MER5B repeat: matches 3. .173 of consensus" 25110. .55213
/note="L2 repeat: matches 2482. .2626 of consensus"
26454. .26782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="12 repeat: matches 112. .316 of consensus"
22706. .22754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="MBR63A repeat: matches 44. .208 of consensus"
17156. .17192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3464. .3770
/note="AluY repeat: matches 1. .309 of consensus"
3996. .4294
                                                                                                                                                                                          'note="MLT1A1 repeat: matches 44. ,315 of consensus"
                                                                                                                                                                                                                                                                                                 /note="L1PA13 repeat: matches 6063. .6156 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                           /note="FLAM_A repeat: matches 1. .130 of consensus"
                                                                                                                                                                                                                                                'note="36 copies 2 mer at 65% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="L2 repeat: matches 1246. .1462 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="L1MB3 repeat: matches 5434, .6176 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="AluJo repeat: matches 1. .301 of consensus"
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                                                         "MIR repeat: matches 51. .157 of consensus" .26447
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                                                                                                                                                                                                                                                                                               116685 bp DNA linear Human DNA sequence from clone 516C23 on chromosome repeat (D6S402) and GSSs, complete sequence. 293021
                  requests: clonerequest@sanger.ac.uk
On Mar 29, 1999 this sequence version replaced gi:3821035.
During sequence assembly data is compared from overlapping clones.
                                                                           Submitted (23-MAR-1999) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humguery@sanger.ac.uk Clone
                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 116685)
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Where differences are found these are annotated as variations
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/note="MERB67A repeat: matches 1. .542 of consensus" 28802. .28943
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/note="LTR16C repeat: matches 259. .387 of
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35717. .35886
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consensus"
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34340. .34703
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30888. .31049
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39973. .41078
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has been finished according to sequence map criteria as follows. attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence is the entire insert of clone 51623. This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      516C23 is from the library RPCI3 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/ VECTOR: pCYPAC2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human chromosome 6, constructed by the Sanger Centre Chromosome
Mapping Group. Further information can be found at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5223. .5418 /note="MLT2E repeat: matches 8. .201 of consensus" 5676. .5798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="L1MB8 repeat: matches 5015. .5445 of consensus"
9728. .10090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="L1PA2 repeat: matches 4981. .6144 of consensus" 12061. .12110
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9021. .9292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="LTR16C repeat: matches 260. .387 of consensus"
7126. .7224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="L1PA12 repeat: matches -1411. .-954 of consensus"
5223. .5418
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3656. .4127
                                                 /note="MIR repeat: matches 9. .248 of consensus"
20472. .20676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4135. .4260
/note="L1PA12 repeat: matches 534. .659 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="L1PA12 repeat: matches 131.
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/db_xref="taxon:9606"
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                                                                                                                        /note="L2 repeat: matches 1706. .1969 of consensus"
                                                                                                                                                               18906.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10094.
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                                                                                                                                                                               /note="L2 repeat: matches 2570. .2698 of consensus"
                                                                                                                                                                                                                                                                                          /note="MLT1B repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                         /note="15 copies 2 mer gt 100% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                   /note="L2 repeat: matches 2655. .2698 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="25 copies 2 mer aa 78% conserved"
                                                                                                                                                                                                                                      'note="L2 repeat: matches 2657.
L2 repeat: matches 627. .842 of consensus" .21698
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                                                                                                                                                                                                                   /note="IS2 transposable element excised from this
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/note="LIR33 repeat: matches 382. .517 of consensus"
34403. .34964
/note="LIMEC_repeat: matches 272. .906 of consensus"
                                                                                                                                 /note="MLT1J repeat: matches 56. .505 of consensus"
42267 .42627
                                                                                                                                                                                                                                                             /note="L2 repeat: matches 1780. .2071 of consensus'
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              'note="71 copies 2 mer tt 63% conserved"
                                                                                                                                                                                                                                                                                                          'note="MIR repeat: matches 12. .120 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note-"L1M4 repeat: matches 3047. .3235 of consensus"
18463. .38837
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37749. .37877
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                                                                                                         note="L2 repeat: matches 2301. .2677 of
                                                                                                                                                                                                                                                                                                                                                                                                                                           note-"L1M4 repeat: matches 3790. .4186 of consensus"
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)5141. .35266
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33887. .34010
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12300. .33151
note="L1PB1 repeat: matches 5323. .6155 of consensus"
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31811. .32018
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24302. .24345
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7125. .37741
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5267. .35587
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14. .39389
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Ge="16 copies 2 mer aa 84% conserved"
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                  Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karattas, A., Klein, J., Leu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Pollara, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC012350 178168 bp DNA linear H' Homo sapiens clone RP11-16N9, WORKING DRAFT SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Birren,B., Linton,L., Nusbaum,C. and Lander,E. Homo sapiens, clone RP11-16N9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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/note="L2 repeat: matches 2180.
54942. .55097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="MIR repeat: matches 49. .210 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="14 copies 2 mer ac 100% conserved" <52243. .>52703
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44166. .44649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note="match: GSS AQ234004" | 4296. .54852
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Pollara, V., Riley, R.,
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Pred. No. 90;
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   Roy, A., Santos, R.,
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Insert size: 176668; sum-of-contigs
Quality coverage: 6.4 in Q20 bases; agarose-fp
Quality coverage: 6.2 in Q20 bases; sum-of-contigs
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1695 1794: gap of 100 bp
1795 4437: contig of 2643 bp in length
4438 4537: gap of 100 bp
4538 6644: contig of 2107 bp in length
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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                                       2 (bases 1 to 180970)
Tomlinson,C., Wohldmann,P., Maupin,R. and Reitz,L.
The sequence of Homo sapiens BAC clone RP11-71J24
                                                                                                               Sulston, J.E. and Waterston, R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
Waterston, R.H.
                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 180970)
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                                                                                                                                                     source
                                                                                                                                                                                                                                                                                                   The RPCI-II human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu)
                                                                                                                                                                                         position 1
RP11-71J24.
                                                                                                                                                                                                                         The clone sequenced to the left is RP11-350124; the clone sequenced to the right is RP11-290A19. Actual start of this clone is at base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence
                                                                                                                                                                                                                                                                        NEIGHBORING SEQUENCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOURCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence, see http://genome.wustl.edu/gsc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (30-SEP-2000) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Aug 28, 2000 this sequence version replaced gi:5732171.
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University School of Medicine, 4444 Forest Park Parkway, St. Louis,
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Submitted (13-AUG-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
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Contact: sapiens@watson.wustl.edu
Summary Statistics
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                                                                                                                                                                                                  ight is RP11-296A19. Actual start of this clone is at base of RP11-71J24; actual end is at base position 180970 of
                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
                                                                                                                                                                  Location/Qualifiers
               /clone="RP11-71J24"
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Local Similarity 90.9%;
                                                                                                                                                                                                                                                                                                                                                                        Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F., Boguslavkiy,L., Boukhgalter,B., Brown,A., Burkett,G., Campoplano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Dewar,
                          Dodge S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand, Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., McCarthy, M., McCarthy, M., McCarthy, M., McPheeters, R., McCarthy, M., M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 6, clone RP11-403120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens chromosome 6 clone RP11-403I20 map 6, WORKING DRAFT
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1 (bases 1 to 182152)
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Meldrim,J., Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J
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46229. .46302
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39561. .39809
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44962. .45131
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Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Banderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F., Boukhgalter,B., Brown,A., Burkett,G., Boguslavkiy,L., Boukhgalter,B., Choepel,Y., Colangelo,M., Collins,S., Campoplano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Jun 4, 2000 this sequence version replaced gi:7655991.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (27-APR-2000) Whitehead Institute/MIT Center for Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
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                                                                                                                                                                                                                                                                                                           * NOTE: This is a 'working draft' sequence. It currently
* consists of 18 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Research,
                                                                                                                                                                                                                                                                as soon as it is available and the accession number will
                                                                                                                                                                                                                               be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 173395 bases at least Q40 Consensus quality: 177417 bases at least Q30 Consensus quality: 179105 bases at least Q20 Insert size: 179000; agarose-fp Insert size: 180452; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality coverage: 4.8 in Q20 bases; agarose-fp Quality coverage: 4.7 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center clone name: 403_I_20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center code: WIBR
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2222: contig of 2222 bp in length
2223 2322: gap of 100 bp
2323 3785: contig of 1463 bp in length
3786 3885: gap of 100 bp
3886 6753: contig of 2868 bp in length
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COMMENT

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note-"assembly_fragment"
58336. .67041
                                                                                                  /note="assembly_fragment"
117731. .138293
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21278. .30240
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101435. .117630
                                                                                                                                                                                                                                                                                                                                                                                       'note-"assembly_fragment"
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76022. .86527
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30341. .40123
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14638. .21177
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10137. .14537
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/db_xref="taxon:9606"
/chromosome="6"
                                    'note="assembly_fragment'
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2323. .3785
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/clone_lib="RPCI-11 Human Male BAC"
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182152: contig of 24211 bp in length
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ORGANISM
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                                                                                                                                                                                                                                                             Sequencing vector: M13, 77%

Sequencing vector: plasmid; 23%
Chemistry: Dye-primer ET; 77% of reads
Chemistry: Dye-terminator Big Dye; 23% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 183385 bases at least Q40
Consensus quality: 185502 bases at least Q30
Consensus quality: 185503 bases at least Q20
Insert size: 197000; agarose-fp
Insert size: 198381; sum-of-contigs
Quality coverage: 4.50 in Q20 bases; sum-of-contigs
Quality coverage: 4.71 in Q20 bases; sum-of-contigs
                                                                                                     * NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    189281 bp DNA linear HTG 07-, HOMO Sapiens chromosome 15 clone RP11-522B15, WORKING DRAFT SEQUENCE, 10 unordered pieces. AC012458 AC012458.4 GI:8570271 HTG; HTGS PHACET ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequencing vector: M13; 77%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (27-007-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center project name: H_NH0522B15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MO 63108, USA On Jun 17, 2000 this sequence version replaced \mathfrak{g}i:6850536.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 189281) Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence of Homo sapiens clone
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                                                                                     be preserved.
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clone_end:T7
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157942. .182152
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4603: contig of 4603 bp in length
4703: gap of unknown length
9761: contig of 5058 bp in length
9861: gap of unknown length
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RESULT 8
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                                                        REFERENCE
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Best Local Similarity
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                                       AUTHORS
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                                                                                                                                                                                                                                                                                                                                                20;
                                       Birren, B., Nusbaum, C.
                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                     Homo sapiens
                                                                                                                                                                   Homo sapiens chromosome 15, clone RP11-522B15, AC087477
                       Homo sapiens chromosome 15, clone RP11-522B15
                                                                                                                                                     AC087477.8
                                                                                                                                                                                                      AC087477
                                                   (bases 1 to 191434)
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89767. .117943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vector_side:right"
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4704. .9761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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39374 c 39106 g 55769 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="RP11-522B15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="assembly_name:Contigl4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="assembly_name:Contig10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="assembly_name:Contig7"
                                                                                                                                                     GI:21844630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89766: gap of unknown tength 117943: contig of 28177 bp in 117944: qap of unknown length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35589: gap of unknown length
51472: contig of 15883 bp in length
51572: gap of unknown length
65229: contig of 13657 bp in length
65329: gap of unknown length
65329: gap of unknown length
89666: contig of 24337 bp in length
                                                                                                                                                                                                                                                                                                                                                               85.5%;
90.9%;
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gap of unknown length
contig of 8550 bp in length
gap of unknown length
contig of 7993 bp in length
                                                                                                                                                                                                                                                                                                                                                               Score 18.8;
Pred. No. 85;
                                         and Lander, E
                                                                                                                                                                                                      191434 bp
                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
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                                                                                                                                                                                                      linear
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AUTHORS
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AUTHORS
COMMENT
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RS Biren, B. Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cocke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Gardyna, S., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Karatas, A., Kells, C., Madonald, P., Major, J., Matthews, C., Lilu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., Murphy, T., Naylor, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Ngyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., O'Connor, J., Peterson, K., Paman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Topham, K., Travers, M., Vassiliev, H., Viel B., Vanne, G., Wanne, G., Vanne, G., Vanne
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Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A.,
Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S.,
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Linazares, R., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K.,
Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N.,
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Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C.,
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H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Petta, R., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Ribback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roya, Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Sougnez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Strauss, N., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Tamber, I., Tamara, A., Talama, J., Young, G., Zainoun, J., Tamber, I., Tamara, A., Talama, J., Young, G., Zainoun, J., Tamber, I., Tamara, A., Talama, J., Tamara, T., Tamara, T., Tamara, A., Talama, J., Tamara, T., Tamara, A., Talama, J., Tamara, T., Tamara, T., Tamara, A., Talama, J., Tamara, T., Tamara,
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Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, S., Farro, S., Ferreira, P., FilzHugh, W., Gage, D., Galagan, J., Bodge, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Karatas, A., LaRocque, K., Lamazares, R., Landers, T., Lande
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Submitted (16-JUL-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Jul 16, 2002 this sequence version replaced 91:20043143.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                             /rpt_family="(TC)n"
/rpt_family="(TC)n"
complement(14459..14464)
/note="430 qual SNGL region"
complement(14475..14479)
/note="430 qual SNGL region"
complement(14493..14498)
/note="430 qual SNGL region"
                       complement(21400. .21579)
/rpt_family="MIR"
                                                                                                                                      complement(20896
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/rpt_family="MIR"
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.0422. .10428
.mote="<30 gual SNGL region"
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/clone_lib="RPCI-11 Human Male BAC"
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3. .21016)
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                                                                                      .ly="(CA)n"
                                                                                                                                              REFERENCE
AUTHORS
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VERSION
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AL772303/c
                                                                  COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                        Db 137915 AAGACTTCTGATTAACAATGAA 137936
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                                                      Submitted (12-JUL-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Jul 14, 2002 this sequence version replaced g1:21540206.
                                                                                                                                                                                                                                                                         197437 bp DNA linear HTG 13-JUL-2002 Mus musculus chromosome 2 clone RP23-185P20, *** SEQUENCING IN PROGRESS ***, 6 unordered pieces.
                           Center: Wellcome Trust Sanger Institute
                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1. (bases 1 to 197437)
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Web site: http://www.sanger.ac.uk
                  Center code: SC
                                                                                                                                 Direct Submission
                                                                                                                                              Almeida, J
                                                                                                                                                                                                           Mus musculus
                                                                                                                                                                                                                              AL772303.3 GI:21748303
HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP
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complement(31951, .31993)
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complement(31104. .31225)
/rpt_family=""AluSp"
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31829. .31851
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31242 .31310
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24327. .24350
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complement(25426. .
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/rpt_family="AluSq"
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complement(22988. .23113)
/rpt_family="L2"
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31760. .31821
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31437. .31741
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complement/20777
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complement/pers
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24471. .24597
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?7835. 2700=
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                                             --- Genome Center
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9, .26667
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                                                                                                                                                                                                    20;
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Mus musculus chromosome UNK clone RP24-381A23, WORKING DRAFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  coverage: 5.99x in Q20 bases; agarose-fp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   as soon as it is available and the accession number will be preserved.
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46843 46942: gap of 100 bp
46943 51200: contig of 4258 bp in length
51201 51300: gap of 100 bp
51301 62621: contig of 11321 bp in length
62622 62721: gap of 100 bp
62722 92981: contig of 30260 bp in length
92982 93081: gap of 100 bp
93082 143175: contig of 50094 bp in length
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                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                     /note="assembly_fragment:00782
fragment_chain:2"
143276. .197437
/note="assembly_fragment:00847"
a 40264 c 38730 g 57970 t
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/chromosome="2"
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fragment_chain:1"
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fragment_chain:1"
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                                                                                                                                                                                                                                                                                                                                                                                                                           /note="assembly_fragment:00220
fragment_chain:2"
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90.9%;
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contig of 54162 k
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                     223761 bp
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                                                                                                                                                                                                                           85;
                                                                                                                                                                                                                                              DB 2; Length 197437;
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                                                                                                                                                                                                                                                                                                           500 others
                       linear
                       HTG 17-JUL-2002
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McPherson, J.D. and Waterston, R.H.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequencing vector: M13; 0% sequencing vector: plasmid; 100% Sequencing vector: plasmid; 100% Chemistry: Dye-primer ET; 0% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 221262 bases at least Q30 Consensus quality: 221869 bases at least Q30 Consensus quality: 222233 bases at least Q30
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McPherson, J.D. and Waterston, R.H.
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Submitted (17-UUL-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
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McPherson, J.D. and Waterston, R.H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          * NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is a rabitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center project name: M_BB0381A23
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Contact: submissions@watson.wustl.edu
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6671
22738
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48422
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2123440
212343
/note="assembly_name:Contig11"
22838. .48321
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                                                                            /note="assembly_name:Contig10"
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                                                                                                                                                                                                                                                                                                     6570: contig of 6570 bp in length
6670: gap of unknown length
22737: contig of 16067 bp in length
22837: gap of unknown length
48321: contig of 25484 bp in length
48421: gap of unknown length
18533: contig of 70112 bp in length
118533: gap of unknown length
118633: gap of unknown length
212339: contig of 93706 bp in length
212339: contig of 3794 bp in length
216333: gap of unknown length
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HTG 05-JUN-2002

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REFERENCE
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Best Local Similarity 90...
20; Conservative
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TITLE
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TITLE
                                                       Query Match
Best Local Similarity
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Submitted (03-APR-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
4 (bases 1 to 229247)
McPherson, J.D. and Waterston, R.H.
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Submitted (05-NOV-2001) Genome Sequencing Center, 4444 Forest Park
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McPherson, J.D. and Waterston, R.H.
The sequence of Mus musculus clone
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammaila; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                            Center project name: M_BA0122N08
                                                                                                                                                                                                                                                                                             Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                         Web site:http://genome.wustl.edu/gsc/index.shtml
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On Apr 3, 2002 this sequence version replaced gi:17105321.
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McPherson, J.D. and Waterston, R.H.
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                                    Conservative
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                                                                                                                                                       /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="RP23-122N8"
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212440. .216233
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118634. .212339
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41598 c 40871 g 69263 t
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                                                     Score 18.8; DB 10; Pred. No. 83;
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                                                                                                                                                                                                                                                                                                                                                                                            Chemistry: Dye-primer ET; 0% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319
Consensus quality: 293243 bases at least Q40 consensus quality: 303369 bases at least Q30 consensus quality: 309642 bases at least Q20 consensus quality: 309642 bases at least Q20 Insert size: 224000; agarose-fp Insert size: 324300; sum-of-contigs quality coverage: 37.21 in Q20 bases; sum-of-contigs quality coverage: 24.94 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                        * NOTE: This is a 'working draft' sequence. It currently consists of 56 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (05-JUN-2002) Genome Sequencing Center, 4444 Forest Parkway, St. Louis, MO 63108, USA
On Jun 5, 2002 this sequence version replaced g1:20069750.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequencing vector: M13; 16%
Sequencing vector: plasmid; 84%
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Contact: submissions@watson.wustl.edu
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McPherson, J.D. and Waterston, R.H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="assembly_name:Contig170"
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109720:
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96704 :
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0: contig of 140165 bp in length
                                                                                                                      Score 18.8; D
Pred. No. 81;
0; Mismatches
                                                                                                                         0;
                                                                                                                                                                                      ВВ
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                                                                                                                            Indels
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KEYWORDS
SOURCE
ORGANISM
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MEDLINE
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Genome Res. 12 (4), 532-542 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Direct Submitted (20-MAR-2002) Center for Genome Research, Whitehead Institute, Nine Cambridge Center, Cambridge, MA 02141, USA
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1 (bases 1 to 10243)
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Methanosarcina acetivorans C2A
Archaea; Euryarchaeota; Methanococci; Methanosarcinales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complete genome.
AE011043 AE010299
AE011043.1 GI:19917413
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                                                                                                                                                                                                                                                         NGEFNRLDVICGHMPKWFVTDLGAMGFEYETVNESTNRKTVRVVRAQTP"
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                                                                                                                    CDS
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REAVELMGKLLDKYGYKSTGETILVADEDEAWYFENCALPDEOYHSAWYAQOYPDGEV
FVAANEFRIRQIEDNRRDIICSELLKPGLKNLGWWNPEDGPLDWLSSYSNGENHPYY
SLRRVWRYLDRVNPDLALSPWTRGFKDVKDGSYAIDYPFSIKPKCPLTLQDVFALYR
SLRRVWRYLDRVNPDLALSPWTRGFKDVKDGSYAIDYPFSIKPKCPLTLQDVFALYR
                            complement(7624. .7914)
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AWWAFDFVSNWARLNYQRWTRVDILPLQQKIETEEVQKTILQWDECCRGKSDLEARDL
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5669. .7393
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                                                                                                                                                                                           DHYEGTQFDLTRGVAAGPYGDPNRFVGPYDGNQNNVTENEHMYGAWERPISIFYQGYT
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4675. .4950
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VKRQALQLYLEGLGFRSIGRFLGVSHVSVQKWIKKFGQEIEELKSENEISIVELDEMH
TYIGNKKNIAGSGLLLLELGKNSSTALLVAEERKLDNYSGKN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGKSVESDVLDLLKGIPEIEYNTPDEVTREIERLESQRTREYTRPEY"
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GGHMHLWKLAEAVKAGINAAGGVPFEFHTVGVCDGIAWGHEGWKYSLDSREIIEDTIE

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MKHRNKELSIFN"
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complement (7624.

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codon_start=

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Methanosarcina acetivorans C2A
Archaea; Euryarchaeota; Methanococci; Methanosarcinales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AE010860 10467 bp DNA linear Methanosarcina acetivorans str. C2A, section 205 c
                                                                                                                                                                                                               Submitted (20-MAR-2002) Center for Genome Research, Whitehead Institute, Nine Cambridge Center, Cambridge, MA 02141, USA
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LMTFIELSGLMIIIYVGIPYLGTVNYFETPSLSGVFEASALIIFAFLGFEDLYRLSGV
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/gene="MA3379"
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FVLLSWIALFSTMNTVLVVMLGGSRIVYGMANSGSLPKILARVHQKLKTPWTAICGIA
FFSSLFVFLGDIATVANIANFMIFIVFFIVNISLIKLRYTDPERKRPFRVPVSIGRFP
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                                                                                                                        organism="Methanosarcina acetivorans C2A"
                                                                                                                                                                                         Location/Qualifiers
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Pred. No. 1.8e+02;
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4511. .4879
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/gene="mtxA"
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/note="MA1804"
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FEGVGAYSAGKLSEAELKRLENLSCAGAGSCAGMFTANTMACMTEALGLSLPGCATAH
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FSNAALHWIKEPKAIETVLKGFLKSLRPEGKLLAQFGGRGNAAEVLLVLMSMLEDEKW
SPYFGNFVFPYGFYGPEEYGKMLKNAGFSVRRAELYSKDMTLKGKEGLSGWFASTWHP
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AVDPKMRVHTGPAKVYDCEEDAMKSILAGDVKPGDIVVIRYEGPKGGPGNEEMLAATA
AIGGMGLLESVALITDGRESGGIRGPCIGHVSPEASEGGPIGLVKDGDLIEINIPERI
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LAHEFGLELPLKTFDELSRTTPHLISLRPGGPNFMLHFDRAGGVEAVVQRLASKLHLD
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EVSESPFLIDSPEGTVRAHASRYVSEIGLADACGIVAGIA
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EVS
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SWQDIQIYMIPDTAFRKKSRNDEPVNSSCIVFAYITAAAWRNLGSFLSYFGPVSPVSH
KTNGMVCFILYYSHYTTPLS"
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REFERENCE
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VERSION
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                        AUTHORS
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                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 15256)

Heilig,R., Petit,J.L., Vico,V., Dasilva,C., Robert,G., Wincker,P., Brottler,P., Cattolico,L., Barbe,V., Pelletier,E., Artiguenave,F., Levy,M., Eckenberg,R., Bruils,T., deBerardinis,V., Cruaud,C., Syapay,G., Saurin,W. and Weissenbach,J. Sequencing of the human chromosome 14
                 Genoscope.
                                                     Unpublished
                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                 UNSOLDSY 152556 bp DNA linear PRI 06-JUN-2001 Human chromosome 14 DNA sequence BAC C-2555016 of library CalTech-D from chromosome 14 of Homo sapiens (Human), complete sequence.
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HTG; HTGS_ACTIVEFIN.
                                (bases 1 to 152556)
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Submitted (06-JUN-2001) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
On Jun 8, 2001 this sequence version replaced g1:12001723.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percentage of bases with a quality value >=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Range
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Overall quality chart :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Assembly program: Phrap; version 2.0 Quality coverage: 6.31x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://www.genoscope.cns.fr/Contact: SeqRef@genoscope.cns.fr
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Identified using the e-PCR software (G. 32591 c 33034 g 42543 t
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Score 18.4; DB 9; Pred. No. 1.4e+02;
             Length 152556;
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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	O	O	Result
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17.2 17.2 16.8 16.8	17.8 17.2	18.4 17.8 17.8	Score
78.2 78.2 76.4 76.4	80.9 78.2	83.6 80.9 80.9	Query
7626 349980 461 21477	1353 513	48908 801 877	Query Match Length DB
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ABL07736 AAH68529 AAC57234 AAK66626	AAC50782 AAK54111	AAK82338 AAC42853 AAO03999	ID
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2000US-0216880.
2000US-0217487.
2000US-0217496.
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2000US-022527

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2000US-0225757

2000US-0225759

2000US-0225759

2000US-0226868

2000US-0226868

2000US-022934

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2000US-0230438

2000US-0230438

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2000US-0230438

2000US-0231244

2000US-0231244

2000US-0231413

2000US-02331413

2000US-02331413
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2000US-0224518.
2000US-0224513.
2000US-0225213.
2000US-0225214.
2000US-0225266.
    2000US-0237039
2000US-0237039
2000US-0237040
2000US-0239933
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2000US-0239937
2000US-0241221
2000US-0241785
2000US-0241785
2000US-0241787
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20-OCT-2000;

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01-NOV-2000;

08-NOV-2000;

17-NOV-2000;

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17-NOV-2000;
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17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
             AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-NOV-2000;
                                                                                                                                                                                                                                                                           Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and
                                                                                                                                                                                                                                                           metastasis
                                                                                                                                                                                                                                                                                                                                            WPI; 2001-483426/52.
                                                                                                                                                                                                                Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                  HUMAN GENOME
                                                                                                                                                                                                                                                               preventing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0241808
2000US-0241808
2000US-0241806
2000US-0246475
2000US-0246475
2000US-0246476
2000US-0246478
2000US-0246524
2000US-0246523
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2000US-0246610
2000US-0246611
2000US-0249211
2000US-02511868
2000US-0251189
2000US-0251199
2000US-0251199
2000US-0251199
                                                                                                                                                                                                                                                                                                                                                                                         Barash SC,
                                                                                                                                                                                                                  SEQ
                                                                                                                                                                                                             ID NO 37150; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                    SCI INC
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RESULT 2
AAC42853
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Best Local 9
             19-APR-1999
21-APR-1999
23-APR-1999
23-APR-1999
28-APR-1999
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23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
01-APR-1999;
06-APR-1999;
08-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                               25-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                    25-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                 EP1033405-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       metabolic pathway; promoter; termination sequence;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3233 GACTTCTGAGTACCAATCAA 3252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana DNA fragment SEQ ID NO: 37100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAC42853;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAC42853 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 48908 BP; 14764 A; 10631 C; 10740 G; 12773 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 GACTTCTGAGTAACAATCAA 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                  2000EP-0301439.
          990S-0128234

990S-0128714

990S-0129845

990S-0130449

990S-0130891

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990S-0132408

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990S-0132486

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990S-0123180
990S-0123548
990S-01235788
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990S-0126785
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95.0%;
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Pred. No. 42
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Mismatches
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12-JUL-1999;
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15-JUL-1999;
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99US-0140893
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990S-0137528

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990S-0139452

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   99US-0161361
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3-0146389.
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RESULT 3
AAQ03999/c
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PR
PR
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DE XXX
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                                                                          RESULT
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Best Local S
Matches 19
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Best Local S
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28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence complementary to dystrophin gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-SEP-1990 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAQ03999;
                                                                                                                                                                                               Paired oligonucleotide primers are used in detecting deletions specifically of the X and Y chromosomes. Dystrophin gene may be isolated this way.
                                                                                                                                                                                                                                                      \begin{array}{lll} \text{Multiplex genomic DNA amplification for deletion detection -} \\ \text{useful for detecting $x$-linked diseases such as ornithine} \\ \text{transcarbamylase deficiency and $x$-linked muscular dystrophy.} \end{array}
                                                                                                                                                                                                                                                                                                                                                                       11-OCT-1989;
                                                                                                                                                                                                                                                                                                                                                                                                            EP364255-A.
                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                               muscular dystrophy; dystrophin; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                       X-chromosome; ornithine transcarbamylase deficiency;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CasKey CT,
                                                                                                                                                                                                                                                                                                                                                                                         18-APR-1990
                                                                                                                                                                              Sequence 877 BP; 289 A; 160 C; 131 G; 297 T; 0 other;
                                                                                                                                                                                                                                     Claim 9; Page 19; 32pp; English.
                                                                                                                                                                                                                                                                                                                                  (BAYU ) BAYLOR UNIV COLLEGE.
                                                                                                                                                                                                                                                                                                                                                     12-0CT-1988;
                                     AAC50782;
                                                       AAC50782 standard; DNA; 1353 BP
                                                                                                                                                                                                                                                                                             WPI; 1990-117752/16.
                                                                                                    Local
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19; Conserv
                                                                                                                                          1 Similarity
19; Conserva
                                                                                                                                                                                                                                                                                                               Chamberlain JS, Gibbs RAL, Rainer JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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99US-0161992.
99US-0161993.
99US-0162142.
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Pred. No. 56;
                                                                                                                                             0;
                                                                                                                                                     Pred. No.
                                                                                                                                                               Score 17.8;
                                                                                                                                             Mismatches
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                                                                                                                                                        56;
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                                                                                                                                                                 DB 11;
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                                                                                                                                                                Length 877;
                                                                                                                                               Indels
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                                                                                                                                                0;
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                                                                                                                                                Gaps
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Arabidopsis thaliana DNA fragment SEQ ID NO: 66116.

18-OCT-2000

(first entry)

0;

XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
Hybridisation protein identi metabolic path Arabidopsis th Ep1033405-A2. 06-SEP-2000. 25-FEB-1999
ni assay; genetic mapping; gene expression control; throat; promocer; termination sequence; ss. thaliana 2000EP-0301439. 990G-0123120. 990G-0123120. 990G-0123120. 990G-0123120. 990G-0123120. 990G-0123120. 990G-0123124. 990G-0123124. 990G-0123124. 990G-0123124. 990G-0123124. 990G-0123124. 990G-0123124. 990G-0123124. 990G-012312. 990G-01231
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23-JUN-1999 22-JUN-1999 22-JUN-1999 29-JUN-1999 30-JUN-1999 30-JUN-1999 30-JUL-1999 30-JU
99US-0140353 99US-0140354 99US-0140695 99US-0141289 99US-0142184 99US-0142184 99US-0142184 99US-0142390 99US-0144005 99US-0144005 99US-0144005 99US-0144005 99US-0144331 99US-0144332 99US-0144333 99US-0144332 99US-0144333 99US-0144334 99US-0144332 99US-0144334 99US-0144332 99US-0144332 99US-0144335 99US-0144335 99US-0144336 99US-0145086 99US-0145087 99US-0145145 99US-0145145 99US-0145145 99US-0145145 99US-0145145 99US-0145145 99US-0146386 99US-0147303 99US-0149368 99US-0149368 99US-0149368 99US-0149368 99US-0149339

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RESULT 5
AAK54111/c
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Best Local
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07-OCT-1999

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13-SEP-1999;
15-SEP-1999;
16-SEP-1999;
20-SEP-1999;
22-SEP-1999;
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21-OCT-1999;
22-OCT-1999;
22-OCT-1999;
25-OCT-1999;
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26-OCT-1999;
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28-OCT-1999;
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29-OCT-1999;
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21-OCT-1999;
21-OCT-1999;
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                  Murine; liver; gene library; amino acid synthesis; binding protein; cell metabolism; energy metabolism; fatty acid metabolism; synthesis; phospholipid metabolism; purine; pyrimidine; nucleoside; nucleotide; replication; transcription; translation; transport protein; ss.
                                                                     Murine transport and binding associated protein encoding cDNA SEQ ID
                                                                                             16-NOV-2001
                                                                                                                                      AAK54111 standard; cDNA; 513
                                                                                                                                                                                         543 AAGACTTCAGAGTCACAATCA 563
                                                                                                                                                                                                    1 AAGACTTCTGAGTAACAATCA 21
                                                                                                                                                                                                                                19;
                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                Conservative
                                                                                            (first entry)
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99US-0156596.
99US-0157117.
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99US-0157865.
99US-0158029.
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99US-0160741.
99US-0160767.
99US-0160768.
99US-0160814.
99US-0160815.
99US-0160980.
99US-0160980.
99US-0161404.
99US-0161406.
99US-0161406.
99US-0161406.
99US-0161359.
99US-0161359.
99US-0161361.
99US-0161393.
99US-0161393.
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99US-0159329.
99US-0159330.
99US-0159331.
99US-0159637.
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99US-0155486.
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99US-0154779.
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99US-0151930.
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99US-0159294.
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                                                                                                                                                                                                                                           90.5%;
                                                                                                                                                                                                                                  0,
                                                                                                                                                                                                                                           Score 17.8;
Pred. No. 5
                                                                                                                                        ВP
                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                      DB
                                                                                                                                                                                                                                                        21;
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RESULT 6
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  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes a novel gene library (A) comprises a gene sequence (or its part) encoding a protein involved in amino acid synthesis, cellular/energy metabolism, metabolism of fatty acids/phospholipids, synthesis or breakdown of purines/pyrimidines/nucleosides/nucleotides, DNA replication/transcription/translation, or is a transport/binding protein. A are produced that correspond to the 3'-end of mRNA but without the polya tail. They can be prepared more efficiently and with less effort than conventional libraries. AAK53436-AAK54275 represent fragments of the gene library described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene library containing sequences with specific 3'-ends and no polyA tail, encoding proteins involved in a wide range of cellular processes {\sf tail},
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 15; Page 205-206; 251pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-368570/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-FEB-2001; 2001DE-2003510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-JUN-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 513 BP; 143 A; 125 C; 107 G; 137 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (LION-) LION BIOSCIENCE AG
                                                                                                                                                                                                                                                                                                                                                                                   ABL07736 standard; cDNA; 7626 BP
                                                                                                                                                                                                                                                                          prosophila; developmental biology; cell signalling;
                                                                                                                                                                                                                                                                                                   Drosophila melanogaster expressed polynucleotide SEQ ID NO 17690
                                                                                                                                                                                                                                                                                                                                                         ABL07736;
New isolated nucleic acid detection reagent for detecting 1000 or more
                           P-PSDB; ABB63633.
                                        WPI; 2001-656860/75.
                                                                   Venter JC, Adams M,
                                                                                         (PEKE ) PE CORP NY
                                                                                                                   23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
                                                                                                                                                            23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                      27-SEP-2001.
                                                                                                                                                                                                               WO200171042-A2
                                                                                                                                                                                                                                       Drosophila melanogaster
                                                                                                                                                                                                                                                                pharmaceutical;
                                                                                                                                                                                                                                                                                                                              26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 22 AAGATTTCTGGGTAACAATAAA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AAGACTTCTGAGTAACAATCAA 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99DE-1058160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78.2%;
86.4%;
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                                                                     PWD,
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                                                                   Myers EW;
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                                                                                                                                                                                                                                                                                 insecticide;
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sequences from the Coryneform bacterium Corynebacterium glutamicum. The are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derive from Coryneform bacterium, and identifying a homologue of a gene derive
                                                                                                                                                                                                                                                             Nakagawa
Tateishi
                                                                                                                                                      mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                      Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing
                                                                              The present invention provides a number of nucleotide and protein
                                                                                                                                                                                                                              WPI; 2001-376931/40.
                                                                                                                                                                                                                                                                                                                                                    16-DEC-1999;
07-APR-2000;
                                                                                                                                                                                                                                                                                                      (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C glutamicum coding sequence fragment SEQ ID NO: 7064.
                                                                                                                                                                                                                                                                                                                                                                                                  18-DEC-2000; 2000EP-0127688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EP1108790-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organic acid synthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAH68529 standard; DNA; 349980 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventueeful in developmental biology and in elucidating cell signalling cell-cell interactions in higher enkaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01816-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAH68529;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   specification,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 17690; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         interactions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ecification, but was obtained in electronic format directly from WIPO ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19;
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                                                                                                            SEQ ID NO: 7064; 246pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                  99JP-0377484.
2000JP-0159162.
2000JP-0280988.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                          Senoh A,
                                                                                                                                                                                                                                                                          Mizoguchi H,
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86.4%;
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derived
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RESULT 8
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                                                                                                                                                                                                          New isolated polynucleotide encoding a plant transcription factor for producing a plant e.g. a woody plant, preferably eucalyptus or pine, having modified gene expression or modified activity of a polypeptide
                                                                                                                                                                          Claim 1; Page 624; 747pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plant; transcription factor; gene expression; eucalyptus; pine; acacia; poplar; sweetgum; teak; mahogany; bzIP; G-box binding factor; basic helix-loop-helix zipper; homeotic; homeodomain; homeobox; MADS; homeodomain zipper; LIM domain; AP2; EREBs; zinc finger domain;
                                                                                                                                                                                                                                                                                                                                                                11-мак-1999;
18-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                      09-MAR-2000; 2000WO-US06112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200053724-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pinus radiata.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        type 2 Cys2His2; CCAAT box element; MYB; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pinus radiata transcription factor DNA sequence #631.
                                                                                                                                                                                                                                                                                                                            (FLET-)
                                                                                                                                                                                                                                                                                                                                          (GENE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAC57234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAC57234 standard; DNA; 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 349980 BP; 82466 A; 95954 C; 90516 G; 81044 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AAGACTTCTGAGTAACAATCAA 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19;
                                                                                                                                                                                                                                                                                                                     FLETCHER CHALLENGE FORESTS LTD.
                                                                                                                                                                                                                                                                                                                                    GENESIS RES & DEV CORP LTD
                                                                                                                                                                                                                                                                                                McGrath A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                            99US-0149485
                                                                                                                                                                                                                                                                                                                                                                             99US-0266513
                                                                                                                                                                                                                                                                                             Shenk MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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Pred. No. 1.
                                                                                                                                                                                                                                                                                            Glenn M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.8e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 349980;
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The present invention relates to novel plant transcription factors from Eucalyptus grandis or Pinus radiata. The present sequence is the coding sequence for one such transcription factor. The transcription factor may be used to produce a plant having modified gene expression such as a woody plant e.g. a eucalyptus, pine, acacla, poplar, sweetgum, teak, or mahogany species or to modify the activity of a polypeptide in a plant. The transcription factors of the present invention are members from the following families of regulatory proteins: bZIP, bZIP family of G-box homeotic/homeodomain/homeobox/MADS, homeodomain zipper, LIM domain, AP2 and EREBS, zinc finger domains of type 2 CysZHis2, CCAAT box elements

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RESULT 9
ANK6626
AXX AAK6
XX AAK6
XX AAK6
XX AAK6
XX Huma
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Best Local Similarity 90.0
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-JAN-2000;

04-FEB-2000;

24-FEB-2000;

24-FEB-2000;

16-MAR-2000;

17-MAR-2000;

17-MAR-2000;

19-MAY-2000;

07-JUN-2000;

28-JUN-2000;

07-JUN-2000;

07-JUL-2000;

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26-JUL-2000;
26-UL-2000;
14-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAK66626 standard; DNA; 21477 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-JAN-2001; 2001WO-US01354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0189874.
2000US-0190076.
2000US-0198123.
2000US-0205515.
2000US-0209467.
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2000US-0220963
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2000US-0226681.
2000US-0226868.
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2000US-0227009.
2000US-0229287.
2000US-0229343.
2000US-0229344.
2000US-0229344.
2000US-0229345.
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2000US-0186350.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 16.8; DB 21;
Pred. No. 1.6e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
              05-SEP-2000;
06-SEP-2000;
06-SEP-2000;
08-SEP-2000;
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29-SEP-2000;
29-SEP-2000;
20-CCT-2000;
02-CCT-2000;
03-NCY-2000;
04-NCY-2000;
08-NCY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-SEP-2000;
25-SEP-2000;
25-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-SEP-2000;
14-SEP-2000;
14-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-SEP-2000;
14-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-SEP-2000;
08-SEP-2000;
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21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-SEP-2000;
                17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0229513
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2000US-0231242
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2000US-0231244
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2000US-023298
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                2000US-0232401

2000US-0232401

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2000US-0233063

2000US-023423

2000US-0234998

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2000US-024674

2000US-0246611

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2000US-0246613

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2000US-0249211

2000US-0249211

2000US-0249211

2000US-0249211
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RESULT 10
AAK66625
ID AAK66
XX
AC AAK66
XX
AC O6-NO
DT 06-NO
XX
DE Human
                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                               ARK54951 to ARK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic corottains and can be used in gene therapy and vaccine production. (I) treatment of diseases associated with inappropriate (I) expression. For certains and polynucleotides may be used in the prevention, diagnosis and cexample, they may be used to treat disorders associated with decreased that affect the activity of (I) by expressions in a patient's genome cuplement the patients own production of (I). Additionally, (I) composed the nucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the cuprotein. (I) proteins and polynucleotides may be used to provent.

CC diagnose and treat immune/haematopoietic antigen genomic to AAR87694 represent human immune/haematopoietic antigen genomic concerns and cancer metastases of haematopoietic antigen genomic concerns and cancer metastas
                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                Query Match
Best Local :
 Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-NOV-2000
01-DEC-2000
01-DEC-2000
05-DEC-2000
05-DEC-2000
05-DEC-2000
06-DEC-2000
08-DEC-2000
08-DEC-2000
08-DEC-2000
                                    06-NOV-2001 (first entry)
                                                                                                                                                                  7221 AGCCTTCTGAGTACCAATCA 7240
                                                                                            AAK66625 standard; DNA; 21480 BP
                                                                                                                                                                                                                                                                           Sequence 21477 BP; 5311 A; 4999 C; 5256 G; 5911 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 21438; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding useful for preventing, metastasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-483426/52.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                             Local
                                                                                                                                                                                   2 AGACTTCTGAGTAACAATCA 21
                                                                                                                                                                                                                        1 Similarity 90.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001US-0259678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0251990
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                                                                                                                                                                                                                                     76.4%; Score 16.8; DB 22; 90.0%; Pred. No. 2.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human immune/hematopoietic antigen polypeptides, diagnosing and/or treating cancers and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ruben SM;
                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                       . 2.3e+02;
                                                                                                                                                                                                                                                 Length 21477;
                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                   0;
14-AUG-2000)
12-AUG-2000)
22-AUG-2000)
22-AUG-2000)
22-AUG-2000)
23-AUG-2000)
23-AUG-2000)
23-AUG-2000)
21-SEP-2000)
01-SEP-2000)
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14-SEP-2000;
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26-JUL-2000;
26-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JUN-2000;
07-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-JUL-2000;
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17-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-MAY-2000;
                                                                 2000US-0232397.
2000US-0232398.
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                                                                                                                                                                                                                                                                                                                      2000US-0226668
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2000US-0229287
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2000US-0226279.
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2000US-0216880
2000US-0217487
2000US-0217496
2000US-0218296
2000US-0218296
2000US-0220964
2000US-0220964
                                                                                                                                                                                               2000US-0231244
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2000US-0209467
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cytostatic; gene therapy; vaccine; metastasis; ds. Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;

17-JAN-2001; 2001WO-US01354

2000US-0180628 2000US-0184664

2000US-0189874. 2000US-0190076. 2000US-0198123.

2000US-0225266. 2000US-0225267. 2000US-0225268. 2000US-0225214

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2000US-0230438

2000US-0232080

S

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2000US-0236368

2000US-0236802

2000US-0237038 2000US-0237039

2000US-0237040. 2000US-0239935.

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RESULT 11
AASO1375/c
ID AASO13
XX AASO13
AC AASO13
AC AASO13
AC Human
DE Human
XX INTERC
KW INT
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05-JAN-2001; 2001US-0259678.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 21437; 3071pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-483426/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7222 AGCCTTCTGAGTACCAATCA 7241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; TANGO 210; clone jthLa152h06; TANGO 364; TANGO 366; dectin-2; INTERCEPT 394; INTERCEPT 400; TANGO 405; cellular process regulator; gene therapy; growth modulator; proliferation; cell differentiation; lymphocyte; bone marrow cell migration; leukaemia; lymphoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 21480 BP; 5315 A; 5005 C; 5257 G; 5903 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human TANGO 405 cDNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-JUL-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAS01375 standard; cDNA; 3114 BP
                                                                                                  mat_peptide
       WO200118016-A1
                                                                                                                                                                  sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         autoimmune disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 76.4%;
Local Similarity 90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 AGACTTCTGAGTAACAATCA 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                         /*tag= 1
298..780
                                                                                                                                                                         /*tag= a
/product= "TANGO 405 protein"
/note= "The ORF is specifically claimed"
154..297
                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                              154..783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             encode the human immune/haematopoietic antigen (I) given in AAM82170 to AAM91921. (I) have cytostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 16.8; DB 22;
Pred. No. 2.3e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 21480;
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2000US-0246525. 2000US-0246526. 2000US-0246527.

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2000US-0246475.
2000US-0246477.

29-SEP-2000 02-OCT-2000; 02-OCT-2000; 02-OCT-2000; 02-OCT-2000; 02-OCT-2000; 13-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 08-NOV-2000; 17-NOV-2000; 18-DEC-2000; 08-DEC-2000; 08-DEC-2000; 08-DEC-2000;

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2000US-0251988. 2000US-0256719. 2000US-0251479. 2000US-0251868. 2000US-0251868. 2000US-0251869.

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RESULT 12
ABA18026
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CC The present sequence encoding for human TANGO 405 protein is isolated CC from cDNA clone jthLa152h06 from a human mixed lymphocyte reaction cDNA CC (AAU00469), TANGO 364 (AAU00471), TANGO 365 (AAU00472), INTERCEPT 394 CC (AAU00473) and INTERCEPT 400 (AAU00476). Novel sequences for murine CC TANGO 210 (AAU00470), INTERCEPT 400 (AAU00477), TANGO 405 (AAU00480) and CC arat INTERCEPT 400 (AAU00478) sequence are also described. The nucleic CC regulating a variety of cellular processes and can be used to express CC murine TANGO 405 proteins show sequence homology to murine dectin-2. CC TANGO 405 proteins show sequence homology to murine dectin-2. CC TANGO 405 modulates growth, proliferation, survival, differentiation, cC activity, morphology and movement/migration of human lymphocytes and CC the marrow cells and tissues and can be used to prevent, diagnose or treat leukaemia, lymphomas and autoimmune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local !
                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                   Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antitheumatic; hepatotropic; cerebroprotective; antiinflammatory;
                                                                                                                             antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal;
antiparasitic; cardiant; immune disorder; cardiovascular disorder;
                      17-JAN-2001; 2001WO-US01334.
                                                 16-AUG-2001.
                                                                          WO200159063-A2
                                                                                                  HOMO sapiens.
                                                                                                                  neurological disease; infection; nephrotropic; gene
                                                                                                                                                                                                                                                                                                                                                               1885 CTTCTGAGTATCAATCAA 1868
                                                                                                                                                                                                                   Human nervous system related polynucleotide SEQ ID NO 10357.
                                                                                                                                                                                                                                                 23-JAN-2002 (first entry)
                                                                                                                                                                                                                                                                               ABA18026;
                                                                                                                                                                                                                                                                                                  ABA18026 standard; DNA; 29329 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3114 BP; 1001 A; 527 C; 517 G; 1069 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; Fig 6A-6C; 326pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated nucleic acid molecules encoding proteins useful as modulating agents in regulating a variety of cellular processes are used for treating e.g. cancer and autoimmune disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-183280/18.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                      5 CTTCTGAGTAACAATCAA 22
                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0393996.
                                                                                                                                                                                                                                                                                                                                                                                                                             74.58;
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Pred. No. 36
                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                 therapy; vaccine;
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21 SEP 2000;
25 SEP 2000;
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26 SEP 2000;
27 SEP 2000;
27 SEP 2000;
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11-SEP-2000
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23-AUG-2000;
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06-SEP-2000;
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04-FEB-2000;
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19-MAY-2000;
                                           2000US-0234998
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2000US-0234223.
2000US-0234274.
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2000US-0232400.
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2000US-0229345
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2000US-0225757
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2000US-0224518.
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2000US-0215135
2000US-0216647
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2000US-0180628.
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2000US-0205515
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2000US-0190076.
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08-NO
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17-NOV-2000;
17-NOV-2000;
useful for preventing, cancers and metastases
        Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases
                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                   Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0249207.
2000US-0249208.
2000US-0249209.
2000US-0249210.
2000US-0249211.
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2000US-0240960.
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2000US-0249213.
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2000US-0246610.
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2000US-0249216.
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ABA2051
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
              18-APR-2000;
19-MAY-2000;
07-JUN-2000;
28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
07-JUL-2000;
                                                                                                                                                  31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
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8110 GACTTCTGAGAAACAATC 8127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 10357; 1701pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Note: The sequence data for this patent did not form populated specification, but was obtained in electronic from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                      Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder; cardiant; immune disorder; cardiovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABA20511;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABA20511 standard; DNA; 29329 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 29329 BP; 6864 A; 6756 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and parasitic infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human nervous system related polynucleotide SEQ ID NO 12842.
                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                         17-JAN-2001; 2001WO-US01334.
                                                                                                                                                                                                                                                                                           16-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                           neurological disease; infection; nephrotropic; gene therapy;
                                                                                                                                     17-MAR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention relates to novel genes (ABA11004-ABA21534) and proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                2000US-0205515.
2000US-0209467.
2000US-0214886.
2000US-0215135.
2000US-0216647.
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                                                                                                                       2000US-0198123.
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                                                                                                                                       2000US-0190076
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2000US-0189874.
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                2000US-0216880
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Pred. No. 3.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7225 G; 8484 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             did not form part of the in electronic format directly
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17-NOV-2000;
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05-DEC-2000;
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06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
         The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune harmolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease militus, autoimmune thyroiditis, diabetes mellitus, Crohn's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-NOV-2000

08-NOV-2000

08-NOV-2000

17-NOV-2000

17-NOV-2000
                                                                                                                                                                                       Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases -
                                                                                                                                                                 Disclosure; SEQ ID NO 12842; 1701pp +
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08-NOV-2000;
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                                                                                                                                                                                                                                                     2001-541565/60.
multiple sclerosis, rheumatoid arthritis and ulcerative
                                                                                                                                                                                                                                                                              Barash SC,
                                                                                                                                                                                                                                                                                                                                2000US-0246478
2000US-0246523
2000US-0246526
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2000US-0246474.
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2000US-0246476.
2000US-0246477.
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                                                                                                                                                              Sequence Listing; English.
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2000US-0222770 2000US-0225757 2000US-0225757 2000US-0225757 2000US-0225759 2000US-0226679 2000US-0226686 2000US-0226686 2000US-0227182 2000US-0227182 2000US-0227909 2000US-0229287 2000US-0229344 2000US-0229344 2000US-0229343 2000US-0229513 2000US-023134 2000US-0231244 2000US-0231244 2000US-0231414 2000US-0231414

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2000US-0232397 2000US-0232398 2000US-0232400 2000US-0232400 2000US-0233063 2000US-0233063 2000US-0233063 2000US-0234023 2000US-0234273 2000US-0234274 2000US-0234274 2000US-0234274 2000US-0234274 2000US-0234274 2000US-0234274 2000US-0234274 2000US-0234274 2000US-0234274

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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
28-JUN-2000)
30-JUN-2000)
07-JUL-2000)
11-JUL-2000)
11-JUL-2000)
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14-JUL-2000]
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04-EEB-2000;
24-EEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
18-MAR-2000;
19-MAY-2000;
07-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 29329 BP; 6864 A; 6756 C; 7225 G; 8484 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-NOV-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
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2000US-0190076.
2000US-0198123.
2000US-0205515.
2000US-0209467.
                                     2000US - 0214886.
2000US - 0215135.
2000US - 0216847.
2000US - 0216880.
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2000US - 022963.
2000US - 0224518.
2000US - 0224519.
2000US - 0225214.
2000US - 0225266.
2000US - 0225266.
2000US - 0225277.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0179065
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94.4%;
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Pred. No. 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .6e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 29329;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
              01-SEP-2000;
01-SEP-2000;
05-SEP-2000;
             29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
20-CCT-2000;
02-CCT-2000;
03-NOV-2000;
04-NOV-2000;
08-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-SEP-2000;
21-SEP-2000;
21-SEP-2000;
25-SEP-2000;
25-SEP-2000;
26-SEP-2000;
27-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-SEP-2000;
12-SEP-2000;
14-SEP-2000;
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08-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-SEP-2000;
06-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-SEP-2000;
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                                                                                                                                                         2000US-0229345
2000US-0229509
2000US-0229519
2000US-0231243
2000US-0231243
2000US-0231243
2000US-0231414
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2000US-0236367
2000US-0246370
2000US-0241786
2000US-0241809
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2000US-0246526
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2000US-0227009.
2000US-0228924.
2000US-0229287.
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2000US-0229344.
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2000US-0246609
2000US-0246610
2000US-0246611
2000US-0246613
2000US-0246513
2000US-0249207
2000US-0249208
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문
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                                                                                                                          cc amino acid sequences given in AAM82170 to AAM91921. (1) have cytostatic cattivity, and can be used in gene therapy and vaccine production. (1) cc proteins and polynuclectides may be used in the prevention, diagnosis and ct treatment of diseases associated with inappropriate (1) expression. For cc example, they may be used to treat disorders associated with decreased cc that affect the activity of (1) by expressing in a patient's genome cc supplement the patients own production of (1). Additionally, (1) cc polynucleotides may be used to produce the secreted (1), by inserting cc polynucleotides may be used to produce the secreted (1), by inserting cc protein. (1) proteins and polynucleotides may be used to provent. (2) cancers and cancer metastases of haematopoietic derived cells. AAK64703 cc sequences from the present inwune/haematopoietic antigen genomic cc represent sequences used in the examplification of the present invention. AAK54942 to AAK54950 and AAM82169 xx
                                                                       Query Match
Best Local :
                                                          Matches
8110 GACTTCTGAGAAACAATC 8127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2000
01-DEC-2000
05-DEC-2000
05-DEC-2000
05-DEC-2000
06-DEC-2000
06-DEC-2000
08-DEC-2000
08-DEC-2000
                                                                                                      Sequence 29329 BP; 6864 A; 6756 C; 7225 G; 8484 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 25603; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                          AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding human immune/hematopoletic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC
                          3 GACTTCTGAGTAACAATC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-NOV-2000;
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                                                          17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Barash SC,
                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0249218
2000US-0249245
2000US-0249245
2000US-0249265
2000US-0249265
2000US-0249297
2000US-0249297
2000US-0249299
2000US-0249299
2000US-0251160
2000US-0250391
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                                                                 74.5%; Score 16.4; DB 22; 94.4%; Pred. No. 3.6e+02;
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                                                    Mismatches
                                                                             Length 29329;
                                                    Indels
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RESULT 15

Gaps

0

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23-AUG-2000

30-AUG-2000

01-SEP-2000

01-SEP-2000

01-SEP-2000

01-SEP-2000

05-SEP-2000

05-SEP-2000

06-SEP-2000

06-SEP-2000

08-SEP-2000

08-SEP-2000
                                                                                                                                                                             14 - AUG - 2000)
15 - AUG - 2000)
22 - AUG - 2000)
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30-JUN-2000;
07-JUL-2000;
                                                                                                                                                                                                                                                                                                 14-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                      11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                 19-MAY-2000;
07-JUN-2000;
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17-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-JAN-2001; 2001WO-US01354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; immune; haematopoletic; immune/haematopoletic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33324.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAK78512;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAK78512 standard; DNA; 29329 BP
                                  2000US-0231244.
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2000US-0225757.
2000US-0225758.
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2000US-0225213.
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2000US-0218290
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                                                                                                                                          2000US-0228924
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                                                                              2000US-0230438
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03-OCT-2000;
04-OCT-2000;
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08-NOV-2000;
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2000US-0246477
2000US-0246477
2000US-0246477
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2000US-0232399
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2000US - 024 9213
2000US - 024 9214
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2000US - 024 9215
2000US - 024 9217
2000US - 024 9217
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2000US-0246613.
2000US-0249207.
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2000US-0246532.
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2000US-0246610.
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2000US-0249265.
2000US-0249297.
2000US-0249299.
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Search completed: March 17, 2003, 10:52:21 Job time: 217.253 secs

Дb

0

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CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic camino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic camino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic camino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic camino acid sequences may be used in the prevention, diagnosis and creatment of diseases associated with inappropriate (I) expression. For cc treatment of diseases associated with inappropriate (I) expression. For cc that affect the activity of (I) by expressing inactive proteins or to cc that affect the activity of (I) by expressing inactive proteins or to cc supplement the patients own production of (I). Additionally, (I) cc polynucleotides may be used to produce the secreted (I), by inserting cc the nucleic acids into a host cell and culturing the cell to express the crocker of the cold treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 cc cancers and cancer metastases of haematopoietic antigen genomic to AAK87994 represent human immune/haematopoietic antigen genomic crepresent sequences used in the exemplification of the present invention.
                                                                          Matches
                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis – \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 33324; 3071pp + Sequence Listing; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rosen CA, Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                            Sequence 29329 BP; 6864 A; 6756 C; 7225 G; 8484 T; 0 other;
Local
                                   3 GACTTCTGAGTAACAATC 20
                                                                          l Similarity
17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0251988.

2000US-0251479.

2000US-0251479.

2000US-0251856.

2000US-0251868.

2000US-0251869.

2000US-0251989.

2000US-0251999.

2000US-0251999.
                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001US-0259678
                                                                                             74.5%;
                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SM;
                                                                                             Score 16.4; DB 22
Pred. No. 3.6e+02;
                                                                              Mismatches
                                                                                                                   DB 22;
                                                                                                                   Length 29329;
                                                                                    0;
                                                                                     Gaps
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Database :
                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence:
                                                                                                                            IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       March 17, 2003, 10:23:12; Search time 777.688 Seconds (without alignments) 458.154 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16154066 seqs, 8097743376 residues
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22
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em_estrl:
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gb_est3:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

o.	ი 5	4	c 3	c 2	c 1	Result
17.8	17.8	17.8	17.8	18.4	18.4	Score
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545	509	418	364	395		•
9	12	14	ø	φ	9	BB
AI738689	BG882650	BQ622226	AA229942	AA837289	AA970603	ID
AI738689 w122a08.x	BG882650 sae94q07.	B0622226 fchlc pk0	AA229942 nc51h06.r	AA837289 od26e07.s	AA970603 op40f09.s	Description

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41622	BG359610	01637	11678	270973	80451	4629	39885	5762	22060	5794	76989	13278	14847	1748	53816	8866	34817	35124	0488	32302	15119	93292	74698	30174	52807	24223	33986	16734	17152	17337	52533	7389	G04045	W69951	F60995	H13851	4670	
16223 RPC1	359610 98C36d01.	16374 uy40b09	116785 uz02c01.	70973 va84c09	30451 AU080451	162943 EST3249	398852 ÉST30935	57625 aq92b06.x	220604 EST2969	579476 ka28d05.	769890 HS_3084	132786 fz68q09.	14847 AU014847	174888 fp54a11	53816 uj06c05.	399883 UI-M-DJ1	348177 uw36b05.	351242 uw93h01.	104881 RPCI-23	323029 maa38b04	151198 uz66c12	932924 EST55281	746982 RPCI-24-	301743 BB30174	528073 BB528073	242233 RPCI-23	339863 EST34392	167340 BJ16734	171523 BJ17152	$173371 \text{ BJ} \overline{17337}$	525332 HS_5226_	738913 gb16	040453 NXSI_108	699516 gb06 <u>F</u> 02	609959 NXSI_053	H138512 ENTNI76	700 vk55a10.	

ALIGNMENTS

FEATURES Source	COMMENT	ĀL	AUTHORS TITLE	REFERENCE		ORGANISM	KEYWORDS	VERSION		DEFINITION	RESULT 1 AA970603/c
Insert Length: 1053 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 344. Location/Qualifiers 1347 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:1579337"	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.	Tumor Gene Index Unpublished (1997)	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),	1 (bases 1 to 347)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia: Eutheria: Primates: Catarrhini: Hominidae: Homo	Homo sapiens	EST.	AA970603.1 GI:3145110	IMAGE:1579337 3', mRNA sequence.	AA970503 347 bp mRNA linear EST 07-JUL-1998 op40f09.sl Soares_NFL_T_GBC_Sl Homo sapiens cDNA clone	

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                               DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP cione distribution found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Insert Length: 1043 Std Error: 0.00 Seq primer: -40ml3 fwd. Er from Amersham High quality sequence stop: 336.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 395)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bonaldo, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA Library Arrayed by: Greg Lennon, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Organ: pooled; Vector: pT773D-Pac (Pharmacia) with /note="Organ: pooled; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "
/clone="IMAGE:1369092"
/clone_lib="NCI_CGAP_GCB1"
                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
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/lab_host="DH10B"
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95.0%;
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Pred. No. 4.1e+02;
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COMMENT

JOURNAL

REFERENCE

TITLE

AUTHORS

SOURCE KEYWORDS ACCESSION /ERSION

ORGANISM

FEATURES

Best Local Similarity

Conservative

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Gaps

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RESULT 2 AA837289/c

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Matches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 616 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D., Michael Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 364)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
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                                                                                                                                /note="Vector: pAMP10; Site_1: Not1; Site_2: ECORI; 1st strand cDNA was primed with oligo(dT)]T of on g of DNAse-treated, total cellular RNA obtained from 5,000-10 000 microdissected cells histologically-determined to brully malignant prostate cancer cells. Double-stranded cDNA was ligated to EcoRI adaptors, 5 cycles of PCR applied to the cDNA with an adaptor-specific primer, and the resulting method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 constructed by Bento Soares and M. Fatima Bonaldo."

<sub>1</sub> 77 c 73 g 145 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1011707"
                                                                                          library was constructed by David Krizman."
82 c 86 g 95 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="45 years old"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="NCI_CGAP_Pr3"
                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83.6%;
95.0%;
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Score 17.8; DB 9;
Pred. No. 7.9e+02;
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Pred. No. 4.3e+02;
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Shoemaker,R., Kelm,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hiller,L., Kucaba,T., Martin,J., Beck,C. Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papillonoldeae; Phaseoleae;
                                                                                                                                                                                                                                                             Glycine max
                                                                                                                                                                                                                                                                                                                                                      sae94907.y1 Gm-c1065 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1065-3758 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2002)
Contact: Freimoser F. M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 418)
Freimoser, F.M., Screen, S., Hu, G. and St. Leger, R.J.
EST analysis of genes expressed by the zygomycete pathogen
Conidiobolus coronatus during optimized secretion of proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fchlc.pk005.h2 Conidiobolus cornatus ARSEF 512 Conidiobolus
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                                                                                                                                                        (bases 1 to 509)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism-"Conidiobolus coronatus"
/strain="ARSEE 512"
/db_xref="taxon:34488"
/clone_lib="Conidiobolus cornatus ARSEE 512"
/note="Vector: UniZap; Conidiobolus coronatus was grown in minimal medium supplemented with Manduca sexta cuticle and peptone for 18 hours. A CDNA library was constructed in the unidirectional Lambda vector UniZap."

a 85 c 76 g 136 t 2 others
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90.5%;
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Pred. No. 8.3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGCCTTGTGAGTAACAATCAA 57
                cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University. Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                           Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                             Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck,
                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 545)
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AI73868.x1 NCI_CGAP_Col6 Homo sapiens cDNA clone IMAGE:2390966 3'similar to TR:054729 054729 BRAIN. ; mRNA sequence.
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                              Tumor Gene Index
                                                                                                                                                                                                                                                                                                      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Shemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2: XhoI; The cDNA library was constructed from mRNA isolated germinating shoots of the cultivar williams. The seeds were allowed to germinate for 24 hours prior to being cold stressed for 2 days at 4C. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-xhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shoemaker."
1 91 c
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/clone="CENOME SYSTEMS CLONE ID: Gm-c1065-3758"
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Gm-c1065"
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Pred. No. 8.9e+02;
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Location/Qualifiers
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Seg primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       580 bp mRNA linear EST 05-AUG-1:
vk55a10.r1 Stratagene mouse Tcell 937311 Mus musculus cDNA clone
IMAGE:958554 5', mRNA sequence.
AA546700
                                                                                                                                                                                                                                                                                                                                                                                                                                     WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,J., Morre,B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                     Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The WashU-HHMI Mouse EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA546700.1 GI:2307991
                                                                                                                                                                                                                                                       High quality sequence stop: 405
                                                                                                                                                                                                                                                                                                          This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     house mouse
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/clone_lib="NCI_CGAP_Col6"
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/lab_host="DH10B"
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/clone_lib="Stratagene mouse Tcell 937311"
/tissue_type="Tcell"
/dev_stage="M30 CD4+ cells"
/lab_host="M30 CD4+ cells"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: blood; Vector: pBluescript SM
                                                                                                                                                                                                     1. .580
                                                                                                                                                     /organism="Mus musculus"
/db_xref="taxon:10090"
                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                               /clone="IMAGE:958554"
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       pBluescript SK-; Site_1:
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                           Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence start: 8 High quality sequence stop: 461.
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Determination of clone end sequences from Entamoeba histolytica
HM1:IMSS sheared DNA library (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Entamoebidae; Entamoeba.
1 (bases 1 to 857)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: M13-Forward Class: shotgun
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Brendan J Loftus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Entamoeba histolytica
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Entamoeba histolytica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: bjloftus@tigr.org
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                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Entameeba histolytica Sheared DNA"
/clone_lib="Entameeba histolytica Sheared DNA"
/note="Vector: pHOS1; Site_1: BSt I; Constructed at The
/note="Vector: pHOS1; Site_1: BSt I; Constructed at The
/note="Vector: pHOS1; Site_1: BSt I; Constructed
/note="Vector: pHOS1; Site_1: BSt I; Constructed At The
/note="Vector: pHOS1; Site_1: Rockville, MD.
/note="Vector: pHOS1; Site_1: BSt I; Constructed At The
/note="Vec
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1. .857
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/strain="HM1:IMSS"
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90.5%;
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Pred. No. 9.3e+02;
          0; Mismatches
                                     Score 17.8;
Pred. No. 1.
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TITLE
                                                                     ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                           ACTTCTGAGTAACAACCAA 150
EST.
Physcomitrella patens.
Physcomitrella patens
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
                                                                                                                                                                                                  gb06f02.y1 Moss EST library PPN Physcomitrella patens cDNA clone PEP_SOURCE_ID:PPN080304 5' similar to TR:Q96538 Q96538 ACYL-COA
                                                                                                                                                                                                                                                 AW699516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: ajohnson@unity.ncsu.edu
Seq primer: T3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    North Carolina State: 919 515 7800 Fax: 919 515 7801
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Contact: Johnson, Arthur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; 1 (bases 1 to 375)
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EST.
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                                                                                                                                    AW699516.1 GI:7583607
                                                                                                                                                             AW699516
                                                                                                                                                                           SYNTHETASE ; , mRNA sequence.
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//lab_host-"XLI-Blue"

//note-"Vector: BlueScript SK; Site_1: Eco RI; Site_2: XhoI

/ The library is from early (spring) wood, taken from
three six-year old trees (three different genotypes), in
the juvenile phase. These trees were induced to form side
wood by bending to a 45 degree angle and tying them to the
ground. Differentiating xylem was harvested from the sides
of the inclined stems, and a mixture of all three
genotypes was used for the library. oligo-dT primed cDNA
was directionally cloned into the EcoRI-xhoI BlueScript SK
vector arms. NOTE: The sequences contain a 'cDNA adapter'
between the EcoRI site and the start of the EST. The
adapter sequence is 'AATTCGGCACGAG'."

80 a 76 c 76 g 129 t 14 others
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/Strain="Coastal plain loblolly pine from North Carolina"
/db_xref="taxon:3352"
/clone="nxSI_053_A10"
/clone_lib="nxSI (Nsf xylem Side wood Inclined)"
/tissue_type="xylem"
/cell_type="Side"
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94.78;
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Pred. No. 1.2e+03;
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Pinus; Pinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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BG040453
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                                                                                                                                               432
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                                                                                                                                               ACTICIGAGIAACCATCAA 414
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,S., Marra,M., Hillier,L., Pape,D., Martin,J., Wylie,T., Underwood
,K., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T.,
K., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T.,
Steptoe,M., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R
, Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: est@watson.wustl.edu
Libraries were constructed by Dr. Stavros Bashiardes as part of the Physcomitrella EST program (PEP) at the Univ. of Leeds (UK) and Washington Univ. in St. Louis (USA) DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Celia Knight (c.d.knight@leeds.ac.uk)
Seq primer: -40RP from Gibco
High quality sequence stop: 405.
Location/Qualifiers
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Ralph Quatrano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
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314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                      Thote—"Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhOI; Construction of the cDNA library was carried out using Stratagenes (IniZAP) - cDNA synthesis kit'. cDNA was constructed using an oligo of primer/linker that contains a XhOI site within it. Following ds cDNA synthesis, EcoRI adapters within it. Following ds cDNA synthesis, EcoRI adapters were ligated to the blunt ends and sample was digested with XhOI. The result is cDNA with an EcoRI sticky end on one side and a XhOI sticky end on the other. This cDNA was ligated directionally in UniZAP arms. The vector is designed containing the pBluescript sequence as well as lambda DNA and cDNA is cloned within this pBluescript sequence. The vector was then packaged using Gold giapackaging extracts. Library was grown in XIIBlue MRF' cells and amplified. The library was grown in XIIBlue exassist as a helper phage that releases the pBluescript sequence and circularises it as single stranded plasmids that are then packaged (by helper phage) and secreted out of the host cell as phagemids. SOLR cells were transformed with phagemids and the library was plated out on LB-amp plates to select for transformants. Approximately 1,000,000 colonies were grown and recovered by using Ouiagen Midi prep kit. 2 micro grams of each library were used to transform DH10B cells by electroporation."
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/clone_lib="Moss EST library PPN"
/tissue_type="protonemata: 7 day old tissue auxin treated"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Physcomitrella patens"
/db_xref="taxon:3218"
                                                                                                                                                                                                                                                                                                                    79.18;
94.78;
                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                     Score 17.4; DB 10;
                                                                                                                                                                                                                                                                                                                        Pred. No. 1.3e+03;
                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                     Length 474;
                                                                                                                                                                                                                                                                                   0
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NXSI_108_D07_F NXSI (Nsf Xylem Side wood Inclined) Pinus taeda cDNA clone NXSI_108_D07 5', mRNA sequence.

477 bp

mRNA

linear

EST 24-JAN-2001

BG040453

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RESULT 12
AW738913/c
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ORIGIN
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AUTHORS
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                                                 TITLE
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                      JOURNAL
                                                                                                                                                                                  AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACTTCTGAGTAACAATCAA 22
                                                               Physcomitrella patens.
Physcomitrella patens
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Eukaryota; Viridiplantae; Funariales; Funariaceae; Physcomitrella.
Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
1 (bases 1 to 549)
1 (bases 1 to 549)
1 (bases 1, Losephola, Come, D., Cuming, A., Knight, C., Clifton, S., Marra, M., Hillier, L., Pape, D., Martin, J., Wylie, T., Underwood, K., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Steptoe, M., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R., Watterston, R. and Wilson, R.
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Contact: Johnson, Arthur
North Carolina State University
Tel: 919 515 7800
Fax: 919 515 7801
                                                                                                                                                                                                                                                                                                                                                                                                                                               AW738913

549 bp mRNA linear EST 25-APR-2000 gb16b06.yl Moss EST library PPN Physcomitrella patens cDNA clone PEP_SOURCE_ID:PPN100912 5' similar to TR:Q96538 Q96538 ACYL-COA
                   Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                            AW738913.1 GI:7647930 EST.
                                                                                                                                                                                                                                                                                                                                                                                                 AW738913
                                                                                                                                                                                                                                                                                                                                                                                                                       SYNTHETASE ;, mRNA sequence.
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1 (bases 1 to 477)
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                                                 Leeds/Wash U Moss EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev_Stage="Juvenile"
//dev_Stage="Juvenile"
//lab_host="XL1-Blue"
//lab_host="XL1-Blue"
//note="vector: BlueScript SK; Site_1: Eco RI; Site_2: XhoI
; The library is from early (spring) wood, taken from
three six-year old trees (three different genotypes), in
the juvenile phase. These trees were induced to form side
wood by bending to a 45 degree angle and tying them to the
ground. Differentiating xylem was harvested from the sides
of the inclined stems, and a mixture of all three
genotypes was used for the library, oligo-dT primed cDNA
was directionally cloned into the EcoRI-XhoI BlueScript SK
vector arms. NOTE: The sequences contain a 'CDNA adapter'
between the EcoRI site and the start of the EST. The
adapter sequence is 'AATTCGGCACGAG'."
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/clone="NXSI_108_D07"
/clone_lib="NXSI (Nsf xylem Side wood Inclined)"
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/cell_type="Side"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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94.78;
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Pred. No. 1.3e+03;
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RESULT 13
AQ525332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
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                                                                                                                                                                                                                                                                                                               AQ525332 608 bp DNA linear GSS 11-MAY HS_5226_B1_C08_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=802 Col=15 Row=F, DNA sequence.
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                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 608)
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Mahairas, G.G., Wallace, J.C., Keller, A., Shaker, R., Furlon
                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                       AQ525332.1
                                                                                                                                                                                                                                                                                 AQ525332
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Location/Qualifiers
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Seq primer: -40RP from Gibco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ,000 colonies were grown and recovered. The double stranded plasmid library was recovered by using Quiagen Midi prep kit. 2 micro grams of each library were used to transform DH10B cells by electroporation."

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/clone_lib="Moss EST library PPN"
/tissue_type="protonemata: 7 day old tissue auxin treated"
/lab_host="DH10B"
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/db_xref="taxon:3218"
                                                                                                                                                                                                                                                          GI:4772652
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94.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 17.4; DB 10;
Pred. No. 1.4e+03;
Furlong, J.,
                             Smith, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            St. Louis, MO 63108, USA
Swartzell,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 549;
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Holzman,T.,Adams,M.D.
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RESULT 14
BJ173371
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                                                                                                                                                                                                                                                                                                            AUTHORS
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                     Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                    Physcomitrella patens subsp. patens.
Physcomitrella patens subsp. patens
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
                                                                                                                                                                                                                Comparison of the moss Physcomitrella patens genome with flowering
                                                                                                                                                                                                                                                                                                  1 (bases 1 to 611)
Fujita, T., Shin-1, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BJ173371 611 bp mRNA linear EST 24-BJ173371 full length cDNA library, chloronemata and young gametophores Physcomitrella patens subsp. patens cDNA clone pph35g12 3', mRNA sequence.
BJ173371
                                                                                                                                                      Unpublished (2002)
Contact: Tadasu Shin-i
                                                                                                                                                                                                        plants genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pleter de Jong
(pleter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
plate: 802 row: F column: 15
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Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: T7
Class: BAC ends
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                                                                                                                                                                                                                                                             jita,T., Shin-1,T., Seki,M., Kamiya,A., Uchiyama,T., Nishiyama,T.
Carninci,P., Hayashizaki,Y., Shinozaki,K., Kohara,Y. and Hasebe
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tshini@genes.nig.ac.jp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anotee "Vector: pBACe3.6; Site_1: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"

123 c 107 g 147 t 10 others
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/sex="male"
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85.7%;
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FEATURES
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BJ171523
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                                                                                      Email: tshini@enes.nig.ac.jp

A backbone of the vector is basically from pBluescript(KS), that was in vivo excised from a modified lPS phage vector (Mo bi Tec, Germany). 5' end of the cDNA that was digested with Xhoi was ligated to Sall site of the vector and the 3' end including polyA tail was ligated to BamHI site of the vector. cDNA instert could k amplified with conventional T7 and T3 primers. This full-length cDNA library was generated basically according to the method described in The Plant J 15, 707-720 (1998) Seki M. et al. Protonemata were blended by the POLYTRON, and then cultivated on the BCDATG medium for 13-14 days under the continuous light.
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BJ171523 full length cDNA library, chloronemata and young gametophores Physcomitrella patens subsp. patens cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2002)
Contact: Tadasu Shin-i
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Physcomitrella patens subsp. patens
Physcomitrella patens subsp. patens
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
1 (bases 1 to 692)
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Fax: 81-559-81-6855
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BJ171523
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/organism="Physcomitrella patens subsp. patens'
/db_xref="taxon:145481"
                                                              1. .692
                                                                                   Location/Qualifiers
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gametophores with 2 to 5 leaves"
1 135 c 128 g 170 t
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/db_xref="taxon:145481"
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94.78;
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